

**11729.1 contg**

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTTGTGTTTGTGTTTGTGTTTGTGTTT  
 GTTTTGAGATGGAGTCTCACTCTGTTGCCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCT  
 CCGCCTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCCGCCAC  
 CACGCTCAGCTAATTTTTTTTGTATTTTAGTAGAGACAGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAA  
 CTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACG  
 CCGGCCCCCAAAGCTGTTTCTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGAC  
 GTGACTGCCAGCAAGCTCAGTCACTCCGTGGTC

**11729-45.21.21.cons1**

TAGGATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGC  
 ATTTAAATATGGGTATTTTCAACTTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTGAGAAGAGATTG  
 AATACCTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAA  
 TCAACTTTGATGACAGTAAAAATGGCCTTTCTGCATGGGAACCTATTGAGCTTATTGGAAATGGACAGTTTA  
 GCAAAGGCATGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTAATGAACCTTATATTAGATGTGT  
 TAAAGCAGGGTTACATGATGAAAAAGGGCCACAGACGGAAAACTGGACTGAAAGATGGTTTGTACTAAAA  
 CCCAACATAATTTCTTACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTTGATGAAAT  
 TGCTGTGTAGAGTCCTTGCCTGACAAAGATGGAAA

**11729-45.21.21.cons2**

TTAGAGAGGCACAGAAGGAAGAAGAGTTAAAAGCAGCAAAGCCGGGTTTTTTTGTGTTTGTGTTTGTGTTTGTGTTT  
 GTTTTGAGATGGAGTCTCACTCTGTTGCCCAAGCTGGAGTACAACGGCATGATCTCAGCTCGCTGCAACCT  
 CCGCCTCCACGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGCCCGCCAC  
 CACGCTCAGCTAATTTTTTTTGTATTTTAGTAGAGACAGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAA  
 CTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACG  
 CCGGCCCCCAAAGCTGTTTCTTTGTCTTTAGCGTAAAGCTCTCCTGCCATGCAGTATCTACATAACTGAC  
 GTGACTGCCAGCAAGCTCAGTCACTCCGTGGTC

**11731.1contig**

TCTTTTCTTTTCGATTTCTTCAATTTGTACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTAT  
 TATAGCTTTCTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTT  
 TCAAGAGCATCTAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTCTGATGACTTTTATGAAGTAACT  
 GATCCCTGAATCAGGTGTGTTACTGAGCTGCATGTTTTTAATCTTTCTGTTTAATAGCTGCTTCTCAGGGACC  
 AGATAGATAAGCTTATTTTGATATTCCTTAAGCTCTTGTTGAAGTTGTTTGATTTCCATAATTTCCAGGTCACA  
 CTGTTTATCCAAAATTTCTAGCTCAGTCTTTGTGTTTGCTTTCTGATTTGGACATCTTGAGTCTGCCTGAG  
 ATCTGCTGATGXTTCCATTCACTGCTTCCAGTTCCAGGTGGAGACTTXXCTTCTGGAGCTCAGCCTGACA  
 ATGCCTTCTTGXTCCCT

**11731.2contig**

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGG  
AGGGCCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACC  
TTCAGGAGGTTACATAACAGGTGATCAAGCCCGTACTTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTT  
AGCTGAAATATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTA  
TGAAACTCATCAAGTTAAAGTTGCAGGGGCCAACAGCTGCCTGTAGTCCTCCCTCCTATCATGAAACAACCCC  
CTATGTTCTCTCCACTAATCTCTGCTCGTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTCATCAGCCAT  
TGCCTCCAGTTGCACCTATAGCAACACCCTTGCTTCTGCTACTTCAGGGACCAGTATTCCTCCCCTAATGA  
TGCCTGCTCCCCTAGTGCCCTTCTGTTAGTA

**11734.1contig**

AATAGATTTAATGCAGAGTGTCAACTTCAATTGATTGATAGTGGCTGCCTAGAGTGCTGTGTTGAGTAGGTT  
TCTGAGGATGCACCCTGGCTTGAAGAGAAAGACTGGCAGGATTAACAATATCTAAAATCTCACTTGTAGGA  
GAAACCACAGGCACCAGAGCTGCCACTGGTGCTGGCACCAGCTCCACCAAGGCCAGCGAAGAGCCCAAAT  
GTGAGAGTGGCGGTGAGGCTGGCACCAGCACTGAAGCCACCCTGGTGCTGGCACTGGCACTGGCACTG  
TTATTGGTACTGGTACTGGCACCAGTGCTGGCACTGCCACTCTTTGGGCTTTGGCTTTAGCTTCTGCTCC  
CGCCTGGATCCGGGGCTTTGGCCCAGGGTCCGATATCAGCTTCGTCAGTTGCAGGGCCCCGGCAGCATTG  
TCCGAGCCGAGCCCAATGCCCATTCGAGCTCTAATCTCGGCCCTAGCCTTGGCTTCAGCTGCAGCCTCAG  
CTGCAGCCTTCAAATCCGCTTCCATCGCCTCTCGGTAC

**11734.2contig**

GCCAAGAAAGCCCCGAAAGGTGAAGCATCTGGATGGGGAAGAGGATGGCAGCAGTGATCAGAGTCAGGCTT  
CTGGAACCACAGGTGGCCGAAGGGTCTCAAAGGCCCTAATGGCCTCAATGGCCCGCAGGGCTTCAAGGG  
GTCCCATAGCCTTTTGGGCCCGCAGGGCATCAAGGACTCGGTTGGCTGCTTGGGCCCGGAGAGCCTTGCT  
CTCCCTGAGATCACCTAAAGCCCGTAGGGGGCAAGGCTCGCCGTAGAGCTGCCAAGCTCCAGTCATCCAA  
GAGCCTGAAGCACCACCACCTCGGGATGTGGCCCTTTTGCAAGGGAGGGCAAATGATTTGGTGAAGTACC  
TTTTGGCTAAAGACCAGACGAAGATTCCCATCAAGCGCTCGGACATGCTGAAGGACATCATCAAAGAATAC  
ACTGATGTGTACCCCGAAATCATTGAACGAGCAGGCTATTCCTTGGAGAAGGTATTTGGGATTCAATTGAAG  
GAAATTGATAAGAATGACCACTTGTACATTCTTCTCAGC

**11736.1contg**

GAGGTCTCACTATGTTGCCAGGCTGTTCTTGAACCTCTGGGATCAAGCAATCCACCCATGTTGGTCTCCA  
AAAGTGCTGGGATCATAGGCGTGAGCCACCTCACCCAGCCACCAATTTTCAATCAGGAAGACTTTTTCTTC  
TTCAAGAAGTGAAGGGTTTCCAGAGTATAGCTACACTATTGCTTGCCTGAGGGTGACTACAAAATTGCTTGC  
TAAAAGGTTAGGATGGGTAAAGAATTAGATTTTCTGAATGCAAAAATAAAATGTGAACATAATGAACTTTAGGT  
AATACATATTCATAAAATAATTATTCACATATTTCTGATTTATCACAGAAATAATGTATGAAATGCTTTGAGTT  
TCTTGGAGTAAACTCCATTACTCATCCCAAGAAACCATATTATAAGTATCACTGATAATAAGAACACAGGAC  
CTTGTCATAAATTCTGGATAAGAGAAATAGTCTCTGGGTGTTTGXTCTTAATTGATAAAATTTACTTGTCCATC  
TTTAGTTTCAAGATCACAAAA

**11736.2contig**

AAGCGGAAATGAGAAAGGAGGGAAAATCATGTGGTATTGAGCGGAAAACCTGCTGGATGACAGGGCTCAGT  
CCTGTTGGAGAACTCTGGGTGGTGCTGTAGAACAGGGCCACTCACAGTGGGGTGCACAGACCAGCACGG  
CTCTGTGACCTGTTTGTACAGGTCCATGATGAGGTAAACAATACACTGAGTATAAGGGTTGGTTTAGAAAC  
TCTTACAGCAATTTGACAAAAGTAATCTTCTGTGCAGTGAATCTAAGAAAAAATTGGGGCTGTATTTGTATGT  
TCCTTTTTTTCATTTTCATGTTCTGAGTTACCTATTTTTATTGCATTTTACAAAAGCATCCTTCCATGAAGGACC  
GGAAGTTAAAAACAAAGCAGGTCCCTTTATCACAGCACTGTCGTAGAACACAGTTTCAGAGTTATCCACCCAAG  
GAGCCAGGGAGCTGGGCTAAACCAAGAATTTTGCTTTTGGTTAATCATCAGGTACTTGAGTTGGAATTGTT  
TTAATCCCATCATTACCAGGCTGGAXGTG

**11739-1&2**

CCGCGGCTCCTGTCCAGACCCTGACCCTCCCTCCCAAGGCTCAACCGTCCCCCAACAACCGCCAGCCTTG  
TACTGATGTGGGCTGCGAGAGCCTGTGCTTAAGTAAGAATCAGGCCTTATTGGAGACATTCAAGCAAAGGT  
TGGACAACTACTTTTCCAGAACAGAAAGGAAAACCTCATGCATCAGAAAAGGTGACTAATAAAGGTACCAGAAG  
AATATGGCTGCACAAATACCAGAATCTGATCAGATAAAACAGTTTAAGGAATTTCTGGGGACCTACAATAAA  
CTTACAGAGACCTGCTTTTTGGACTGTGTTAGAGACTTCACAACAAGAGAAGTAAACCTGAAGAGACCACC  
TGTTTCAAGAACATTGCTTACAGAAATATTTAAAAATGACACAAAGAATATCCATGAGATTTTCAAGGAATATCATA  
TTCAGCAGAATGAAGCCCTGGCAGCCAAAGCAGGACTCCTTGGCCAACACGATAGAGAAGTCCTGATGG  
ATGAACTTTTGTGAAAGATTGCCAACAGCTGCTTTATTGGAAATGAGGACTCATCTGATAGAATCCCCTGA  
AAGCAGTAGCCACCATGTTCAACCATCTGTCATGACTGTTTGGCAAATGGAAACCGCTGGAGAAACAAAATT  
GCTATTTACCAGGAATAATCACAATAGAAGGTCTTATTGTTTCAAGTAAATAATAAGATGCAACATTTGTTGAG  
GCCTTATGATTCAGCAGCTTGGTCACTTGATTAGAAAAATAAACCATTTGTTTCTTCAATTGTGACTGTTAATTT  
TAAAGCAACTTATGTGTTTCGATCATGTATGAGATAGAAAAATTTTTATTACTCAAAGTAAAAATAAATGGA

**11740.1.contig**

GAAAAAAAATATAAAACACACTTTTTGCGAAAACGGTGGCCCTAAAAGAGGAAAAAGAATTTACCAATATAAAT  
CCAATTTTATGAAAACGACAATTTAATCCAAGAATCACTTTTGTAATGAAGCTAGCAAGTGATGATATGAT  
AAAATAAACGTGGAGGAAATAAAAAACACAAGACTTGGCATAAGATATATCCACTTTTGATATTAACTTGTGA  
AGCATATTCTTCGACAAATTGTGAAAGCGTTTCTGATCTTGCTTGTCTCCATTTCAAATAAGGAGGCATATC  
ACATCCCAAGAGTAACAGAAAAAGAAAAAGACATTTTTGCATTTTGAGATGAACCAAAGACACAAAAACAA  
ACGAACAAAGTGTCATGTCTAATTCTAGCCTCTGAAATAAACCTTGAACATCTCCTACAAGGCACCGTGATT  
TTTGTAATTCTAACCTGAAGAAATGTGATGACTTTTGTGGACATGAAAATCAGATGAGAAAACTGTGGTCTTT  
CCAAAGCCTGAACTCCCCTGAAAACCTTTGCA

**11766.1.contig**

CTGGGATCATTCTCTTGATGTCATAAAAGACTCTTCTTCTCCTCTTCATCCTCTTCTTCATCCTCTTCTGTA  
CAGTGCTGCCGGGTACAACGGCTATCTTTGTCTTTATCCTGAGATGAAGATGATGCTTCTGTTTCTCCTACC  
ATAACTGAAGAAATTCGCTGGAAGTCGTTTGAAGTGGCTGTTTCTCTGACTTCACCTTCTTTGTCAAACCTGA  
GTCTTTTACCTCATGCCCCCAGCTTCCACAGCATCTTCATCTGGATGTTTATTTTCAAAGGGCTCACTGA  
GGAAACTTCTGATTCAGAGGTCGAAGAGTCACTGTGATTTTCTCCTCATTTTGTCTGCAAATTTGCCTCTTTG  
CTGTCTGTGCTCTCAGGCAACCCATTTGTTGTCATGGGGGCTGACAAAGAAACCTTTGGTTCGATTAAGTGG  
CCTGGGTGTCCCAGGCCCATTTATATTAGACCTCTCAGTATAGCTTGGTGAATTTCCAGGAAACATAACACC  
ATTCATTCGATTTAACTATTGGAATTGGTTT

**11766.2.contig**

GAGGGTTGGTGGTAGCGGCTTGGGGAGGTGCTCGCTCTGTGGTCTTGCTCTCTCGCACGCTTCCCCCGG  
CTCCCTTCGTTTCCCCCCCCCGGTGCGCTGCGTGCCGGAGTGTGTGCGAGGGAGGGGGAGGGCGTCCG  
GGGGGTGGGGGGAGGCGTTCGGTCCCCAAGAGACCCGCGGAGGGAGGCGGAGGCTGTGAGGGACTCC  
GGGAAGCCATGGACGTCGAGAGGCTCCAGGAGGCGCTGAAAGATTTTGAGAAGAGGGGGAAAAAGGAAG  
TTTGTCTGTCTGGATCAGTTTCTTTGTCATGTAGCCAAGACTGGAGAAACAATGATTCAGTGGTCCCAAT  
TTAAAGGCTATTTTATTTTCAAACCTGGAGAAAGTGATGGATGATTTCAGAACTTCAGCTCCTGAGCCAAGAG  
GTCCTCCCAACCCTAATGTCTGA

**11773.2.contig**

AAGCAGGCGGCTCCCGCGCTCGCAGGGCCGTGCCACCTGCCCGCCCGCCCGCTCGCTCGCTCGCCCGC  
CGCGCCGCGCTGCCGACCGCCAGCATGCTGCCGAGAGTGGGCTGCCCGCGCTGCCGXTGCCG

**11775-1&2**

ATCTCTTGATGCCAAATATTTAATATAAATCTTTGAAACAAGTTCAGATGAAATAAAAATCAAAGTTTGCAAA  
AACGTGAAGATTAACCTAATTGTCAAATATTCCTCATTGCCCAAATCAGTATTTTTTTTATTTCTATGCAAAA  
GTATGCCTTCAAACCTGCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCAT  
CTTGCAATTGTAAGAAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACACACAGTGTGC  
ACGCCAATGACAAAAACAATTTGGCCTCTCCTAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGG  
GAACACTGTGTACCCCTCCCTACAATCCAGGTAGTTTCTTTAATCCAATAGCAAATCTGGGCATATTTGA  
GAGGAGTGATTCTGACAGCCACGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCCTGAA  
AAAATGCCAATAATTTTTCGCTCCCACTTCTGCTGCTGCTCTTCCACATCCTCACATAGACCCAGACCCGC  
TGGCCCTGGCTGGGCATCGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTCACAGAAGCG  
ATACACCAAATTGCCTGGTCGGTCATTGTCATAACCAGAGA

**11777.1&2.cons**

CAGACGGGGTTTCACTATGTTGGCTAGGCTGGTCTTGAACCTCCTGACTTCAGGTGATCTGCCTGCCTTGGC  
CTCCCAAAGTGCTGGGATTACAGGCATAAGCCACTGCGCCCGGCTGATCTGATGGTTTCATAAGGCTTTTC  
CCCCTTTTGCTCAGCACTTCTCCTTCCTGCGCCATGTGAAGAAGGACATGTTTGCTTCCCCTTCCACCACG  
ATTGTAAGTTGTTTCTGAGGCCTCCCCGGCCATGCTGAACTGTGAGTCAATTAAACCTCTTTCCTTTATAAA  
TTATCCAGTTTTGGGTATGTCTTTATTAGTAGAATGAGAACAGACTAATACAACCCTTAAAGGAGACTGACG  
GAGAGGATTCTTCTGGATCCCAGCACTTCTCTGAATGCTACTGACATTCTTCTTGAGGACTTTAAACTGG  
GAGATAGAAAACAGATTCCATGGCTCAGCAGCCTGAGAGCAGGGAGGGAGCCAAGCTATAGATGACATGG  
GCAGCCTCCCCTGAGGCCAGGTGTGGCCGAACCTGGGCAGTGCTGCcACCCACCCCACCAGGGCCAAGT  
CCTGTCTTGAGAGCCAAGCCTCAATCACTGCTAGCCTCAAGTGTCCCCAAGCCACAGTGGCTAGGGGG  
ACTCAGGGAACAGTTCAGTCTGCCCTACTTCTCTTACCTTTACCCCTCATACCTCCAAAGTAGACCATGT  
TCATGAGGTCCAAAGG

**11779.2.contig**

AAGCGAGGAAGCCACTGCGGCTCCTGGCTGAAAAGCGGCGCCAGGCTCGGGAACAGAGGGAACGCGAAG  
AACAGGAGCGGAAGCTGCAGGCTGAAAGGGACAAGCGAATGCGAGAGGAGCAGCTGGCCCGGGAGGCT  
GAAGCCCGGGCTGAACGTGAGGCCGAGGCGCGGAGACGGGAGGAGCAGGAGGCTCGAGAGAAGGCGCA  
GGCTGAGCAGGAGGAGCAGGAGCGACTGCAGAAGCAGAAAGAGGAAGCCGAAGCCCGGTCCCGGGAAG  
AAGCTGAGCGCCAGCGCCAGGAGCGGGAAAAGCACTTTCAGAAGGAGGAACAGGAGAGACAAGAGCGAA  
GAAAGCGGCTGAGGAGATAATGAAGAGGACTCGGAAATCAGAAGCCGCCGAAACCAAGAAGCAGGATGC  
AAAGGAGACCGCAGCTAACAATTCCGGCCCAGACCCTTGTGAAAGCTGTAGAGACTCGGCCCTCTGGGCT  
TCCAGAAAGGATTCTATTGCAGAAAGGAAGGAGCTXGGCCCCCAXGGA

**11781 & 37.cons**

CTCTGTGGAAAACCTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCT  
GATTACTGCAACACAGAGAACGAAGAAGAACTTTTCTCATACAGGATCAGCAGGGCCTCATCACTGGG  
CTGGATTCATACTACCCACACAGACCGCGTTTCTCTCCAGTGTCGACCTACACACTCACTGCTCTTACCA  
GATGATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCCAGGAAACTGGATTCTTTAACTAAC  
TGACCATGGACTAGAGGAGATTTCTTCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTC  
TGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTT  
GAGTCCAACACCTTCCAAGAACAACAAACCATATCAGTGTACTGTAGCCCCCTTAATTTAAGCTTTCTAGAAA  
GCTTTGGAAGTTTTTGTAGATAGTAGAAAGGGGGGCATCACXTGAGAAAGAGCTGATTTTGTATTTAGGTT  
TGAAAAGAAATAACTGAACATATTTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAA  
CTCAGAAATTAAGTTACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCATATA  
CCCTTCCTTCTGGATTCACCAATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTAATTTCA  
ATTTGTTTATATTTACCTCTGGGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTT  
TGGATTTTCTGTGGTTTATGGCAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTG  
ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTTCA  
GATATTTTCTCTACAATAAAGTAACAAT

**11781-76-87-37**

CTCTGTGGAAACTGATGAGGAATGAATTTACCATTACCCATGTTCTCATCCCCAAGCAAAGTGCTGGGTCT  
GATTACTGCAACACAGAGAACGAAGAAGAACTTTTCCTCATACAGGATCAGCAGGGCCTCATCACACTGGG  
CTGGATTCACTACCCCCACACAGACCGCGTTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACCA  
GATGATGTTGCCAGAGTCAGTAGCCATTGTTTGCTCCCCAAGTTCCAGGAAACTGGATTCTTTAACTAAC  
TGACCATGGACTAGAGGAGATTTCTTCCTGTGCGCCAGAAAGGATTTTCATCCACACAGCAAGGATCCACCTC  
TGTTCTGTAGCTGCAGCCACGTGACTGTTGTGGACAGAGCAGTGACCATCACAGACCTTCGATGAGCGTTT  
GAGTCCAACACCTTCCAAGAACAACAAACCATATCAGTGTACTGTAGCCCCTTAATTTAAGCTTTCTAGAAA  
GCTTTGGAAGTTTTGTAGATAGTAGAAAGGGGGGCATCACCTGAGAAAGAGCTGATTTTGTATTTACAGTT  
TGAAAAGAAATAACTGAACATATTTTTAGGCAAGTCAGAAAGAGAACATGGTCACCCAAAAGCAACTGTAA  
CTCAGAAATTAAGTTACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGAATGGTATAATGAACCCCCATATA  
CCCTTCCTTCTGGATTCACCAATTGTTAACATTTTTTCTCTCAGCTATCCTTCTAATTTCTCTCTAATTTCA  
ATTTGTTTATATTTACCTCTGGGCTCAATAAGGGCATCTGTGCAGAAATTTGGAAGCCATTTAGAAAATCTTT  
TGGATTTTCCTGTGGTTTATGGCAATATGAATGGAGCTTATTACTGGGGTGAGGGACAGCTTACTCCATTTG  
ACCAGATTGTTTGGCTAACACATCCCGAAGAATGATTTTGTGAGGAATTATTGTTATTTAATAAATATTTTCA  
GATATTTTCTCTACAATAAAGTAACAATTA

**11784-1 & 2**

GGACGACAAGGCCATGGCGATATCGGATCCGAATTCAAGCCTTTGGAATTAATAAACCTGGAACAGGGAA  
GGTGAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGTGCACAGTTGAATGGGAAGTGTGGGTTT  
AGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAGTGGTGGGAGGTCAAGTGGGGAAGTTGGT  
GAATGTGGAATAACTTACCTTTGTGCTCCACTTAAACCAGATGTGTTGCAGCTTTCCTGACATGCAAGGATC  
TACTTTAATTCACACTCTCATTAAATAAATTGAATAAAAGGGAATGTTTTGGCACCTGATATAATCTGCCAGG  
CTATGTGACAGTAGGAAGGAATGGTTTCCCCTAACAAAGCCCAATGCACTGGTCTGACTTTATAAATTATTTA  
ATAAAATGAACTATTATC

**11785.2.contig**

GGCAGTGACATTCACCATCATGGGAACCACCTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCAC  
CCAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCTA  
AGGTGCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAAAC  
TTTCTAATTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAAA  
CTGGTGTTACCCAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAAAACAGGATGTG  
CTTTCCTTTGCCATTTAGGGTTTCTTCTCTTTCTTTCTTTATTAACCACT

**11718-1&2 cons**

TGCGCTGAAAACAACGGCCTCCTTTACTGTAAAATGCAGCCACAGGTGCTTAGCCGTGGGCATCTCAACC  
ACCAGCCTCTGTGGGGGGCAGGTGGGCGTCCCTGTGGGCCTCTGGGCCCACGTCCAGCCTCTGTCCTCT  
GCCTTCCGTTCTTCGACAGTGTCCCGGCATCCCTGGTCACTTGGTACTTGGCGTGGGCCTCCTGTGCTGC  
TCCAGCAGCTCCTCCAGGXGGTCGGCCCGCTTACCAGCAGCCTCATGTTGTGTCCGGAGGCTGCTCACGG  
CCTCCTCCTTCCTCGCGAGGGCTGTCTTACCCTCCGGXGCACCTCCTCCAGCTCCAGCTGCTGGCGGGC  
CTGCAGCGTGGCCAGCTCGGCCTTGGCCTGCCGCGTCTCCTCCTCARAGGCTGCCAGCCGGTCTCGAA  
CTCCTGGCGGATCACCTGGGCCAGGTTGCTGCGCTCGCTAGAAAGCTGCTCGTTACCCGCCTGCGCATCC  
TCCAGCGCCCGCTCCTTCTGCCGCACAAGGCCCTGCAGACGCAGATTCTCGCCCTCGGCCTCCCAAGCT  
GGCCCTTCACTCCGAGCACCGCTCCTGAAGCTTCCGCTCCGACTGCTCCAGCTCGGAGAGCTCGGCCTC  
GTACTTGTCCCGTAAGCGCTTGATGCGGCTCTCGGCAGCCTTCTCACTCTCCTCCTTGGCCAGCGCCATGT  
CGGCCTCCAGCCGGTGAATGACCAGCTCAATCTCCTTGTCCCGGCCTTCCGGATTCTTCCCTCAGCTCC  
TGTTCCCGGTTTCAAGCAGCCACGCTCCTCCTTCTGCTGCGGCCGGCCTCCACGCCTGCCTCTCCAGCT  
CCAGCTGCTGCTTCAGGGTATTCAGCTCCATCTGGCGGGCCTGCAGCGTGGCCA

**13690.4**

CAACTTATTACTTGAAATTATAATATAGCCTGTCCGTTTGCTGTTTCCAGGCTGTGATATATTTTCTAGTGG  
TTTGACTTTAAAAATAAATAAGGTTTAATTTTCTCCCC

**13693.1**

TGCAAGTCACGGGAGTTTATTTATTTAATTTTTTTTCCCCAGATGGAGACTCTGTGCCCCAGGCTGGAGTGCA  
ATGGTGTGATCTTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCACAGCCTCCCGA  
GTAGCTGGGATTACAGGTGCCCGCCACCACACCCAGCTAATTTTTATTTTTTAGTAAAGACAGGGTTTCCC  
CATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCCACCTGCCTCGGCCTCCCAAAGTGTTGG  
GATTACAGGCGTGAGCTACCCGTGCCTGGCCAGCCACTGGAGTTTAAAGGACAGTCATGTTGGCTCCAGC  
CTAAGGCGGCATTTTCCCCCATCAGAAAGCCCGCGGCTCCTGTACCTCAAATAGGGCACCTGTAAAGTCA  
GTCAGTGAAGTCTCTGCTCTAACTGGCCACCCGGGGCCATTGGCNTCTGACACAGCCTTGCCAGGANGCC  
TGCATCTGCAAAGAAAAGTTCACTTCCTTTCCG

**13694.1**

CAGAGAATCTKAGAAAGATGTCGCGTTTTCTTTTAAATGAATGAGAGAAGCCCATTTGTATCCCTGAATCATTG  
AGAAAAGGCGGCGGTGGCGACAGCGGCGACCTAGGGATCGATCTGGAGGGACTTGGGGAGCGTGCAGA  
GACCTCTAGCTCGAGCGCGAGGGACCTCCCGCCGGGATGCCTGGGGAGCAGATGGACCCTACTGGAAGT  
CAGTTGGATTCAATTTCTCTCAGCAAGATACTCCTTGCCTGATAATTGAAGATTCTCAGCCTGAAAGCCAG  
GTTCTAGAGGATGATTCTGGTTCTCACTTCAGTATGCTATCTCGACACCTTCTAATCTCCAGACGCACAAA  
GAAAATCCTGTGTTGGATGTTGNGTCCAATCCTTGAACAAACAGCTGGAGAAGAACGAGGAGACCGGTAAT  
AGTGGGTTCAATGAACATTTGAAAGAAAACCAGGTTGCAGACCCTG

**"REPLACEMENT SHEETS"**

**13694.2**

GACTGTCCTGAACAAGGGACCTCTGACCAGAGAGCTGCAGGAGATGCAGAGTGGTGGCAGGAGTGGAAG  
CCAAAGAACACCCACCTTCTCCCTTGAAGGAGTAGAGCAACCATCAGAAGATACTGTTTTATTGCTCTGGT  
CAAACAAGTCTTCTGAGTTGACAAAACCTCAGGCTCTGGTGAATTCTGAATCTGCAGTCCACTTTCCATAA  
GTTCTTGTGCAGACAACCTGTTCTTTGCTTCCATAGCAGCAACAGATGCTTTGGGGCTAAAAGGCATGTCCT  
CTGACCTTGCAGGTGGTGGATTTTGTCTTTTACAACATGTACATCCTTACTGGGGCTGTGCTGTCACAGGGA  
TGTCTTGTGCTGGACTGTTCTGCTATGGGGATATCTTCGTTGGACTGTTCTTCATGCTTAATTGCAGTATTAG  
CATCCACATCAGACAGCCTGGTATAACCAGAGTTGGTGGTTACTGATTGTAGCTGCTCTTTGTCCACTTCAT  
ATGGCACAAGTATTTTCTCAACATCCTGGCTCTGGGAAG

**13695.1**

GAAATGTATATTTAATCATTCTCTTGAACGATCAGAACTCTRAAATCAGTTTTCTATAACARCATGTAATACAG  
TCACCGTGGCTCCAAGGTCCAGGAAGGCAGTGGTTAACACATGAAGAGTGTGGGAAGGGGGCTGGAAACA  
AAGTATTCTTTTCTTCAAAGCTTCATTCTCAAGGCCTCAATTCAAGCAGTCATTGTCTTGTCTTTCAAAG  
TCTGTGTGTGCTTCATGGAAGGTATATGTTTGTTCCTTAATTTGAATTGTGGCCAGGAAGGGTCTGGAGAT  
CTAAATTCAGAGTAAGAAAACCTGAGCTAGAACTCAGGCATTTCTCTTACAGAACTTGGCTTGCAGGGTAGA  
ATGAANGGAAAGAACTTAGAAGCTCAACAAGCTGAAGATAATCCCATCAGGCATTTCCCATAGGCCTTGCA  
ACTCTGTTCACTGAGAGATGTTATCCTG

**13695.2**

AGTCTGGAGTGAGCAAACAAGAGCAAGAAACAARRAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGA  
TAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGAGTG  
ATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGG  
GAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGA  
GGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAGTATGTACCC  
TAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGTCAAATGATT  
CACTTTTTATGATGCTTCCCAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCCAAGTTGAGAAAAAT  
GATCATAATTTTAGCATAAACCGAGCAATCGGCGACCCC

**13697.1**

TAGCTGTCTTCTCACTCTTATGGCAATGACCCCATATCTTAATGGATTAAGATAATGAAAGTGTATTTCTTA  
CACTCTGTATCTATCACCAGAAGCTGAGGTGATAGCCCGCTTGTCAATTGTCATCCATATTCTGGGACTCAGG  
CGGGAACCTTTCTGGAATATTGCCAGGGAGCATGGCAGAGGGGCACAGTGCATTCTGGGGGAATGCACATT  
GGCTCAGCCTGGGTAATGAGTGATATACATTACCTCTGTTCACTCACTCATTGCCAGCACCAGTCACAAGG  
CCCCACCAAATACCAGAGCCCAAGAAATGTAGTCCTGTTGATATGGTTTTGCTGTGTCCCAACCCAAATCTC  
ATCTTGAATTGTAAGCTCCCATAATTCCCATGTGTTGTGGGAGGGACCTGGTG





**13705.2**

TGGGGCGGAAAGAAGCCAAGGCCAAGGAGCTGGTGCGGCAGCTGCAGCTGGAGGCCGAGGAGCAGAGG  
AAGCAGAAGAAGCGGCAGAGTGTGTCCGGCCTGCACAGATACCTTCACTTGCTGGATGGAAATGAAAATTA  
CCCGTGTCTTGTGGATGCAGACGGTGATGTGATTTCTTCCCACCAATAACCAACAGTGAGAAGACAAAGG  
TTAAGAAAACGACTTCTGATTTGTTTTGGAAGTAACAAGTGCCACCAGTCTGCAGATTTGCAAGGATGTCA  
TGGATGCCCTCATTCTGAAAATGGCAAGAAATGAAAAAGTACACTTTAGAAAATAAAGAGGAAGGATCACTC  
TCAGATACTGAAGCCGATGCAGTCTCTGGACAACCTTCCAGATCCCAACGAATCCCAGTGCTGGAAAGGA  
CGGGCCCTTCTTCTGGTGGTGGAACANGTCCCGGTGGTGGATCTTGAANGGAACCTGAANGTGGTGTA  
CCCCGTCCAAGGCCGACCTTGGCCAC

**13707.4**

TCCCGCGCTCGCAGGGCNCGTGCCACCTGCCYGTCCGCCCGCTCGCTCGCTCGCCCGCCGCGCCGCGC  
TGCCGACCGYACAGATGCTGCCGAGAGTGGGCTGCCCGCGCTGCCGCTGCCGCGCCGCGCGCTGCTG  
CCGCTGCTGCCGCTGCTGCTGCTGC

**13708.1&2**

GGCGGGTAGGCATGGAAGTGAAGAAGCAAGAAGCTTTCAGACTACGTGGGGAAGAATGAAAAACCAA  
AATTATCGCCAAGATTCAGCAAAGGGGACAGGGAGCTCCAGCCCGAGAGCCTATTATTAGCAGTGAGGAG  
CAGAAGCAGCTGATGCTGTAATACAGAAAGACAAGAGGAGCTCAAGAGATTGGAAGAAAATGATGATGA  
TGCCTATTTAACTCACCATGGGCGGATAACACTGCTTTGAAAAGACATTTTCATGGAGTGAAAGACATAAA  
GTGGAGACCAAGATGAAGTTCACCAGCTGATGACACTTCCAAAGAGATTAGCTCACCT

**13709.1**

TCTGAAGGTAAATGTTTCATCTAAATAGGGATAATGRTAAACACCTATAGCATAGAGTTGTTTGAGATTAAA  
TGAGATAATACATGTAAAATTATGTGCCTGGCATAACAGCAAGATTGTTGTTGTTGTTGATGATGATGATG  
ATGATAATATTTTTCTATCCCCAGTGCACAACCTGCTTGAACCTATTAGATAATCAATACATGTTTCTTGAAGT  
AGATCAATTTCCCATGTTGTCTGACTGATGAAGCCCTACATTTTCTTCTAGAGGAGATGACATTTGAGCAA  
GATCTTAAAGAAAATCAGATGCCTTCACCTGACCACTGCTTGGTATCCCATGGCACTTTGTACATCTCTCC  
ATTAGCTCTCATCTCACCAGCCCATCATTATTGTATGTGCTGCCTTCTGAAGCTTGCAGCTGGCTACCATCM  
GGTAGAATAAAAATCATCCTTTCATAAAATAGTGACCCTCCTTTTTTATTTGCATTTCCCAAAGCCAAGCACC  
GTGGGANGGTAG

**13709.2**

TATGAAGAAGGGAAAAGAAGATAATTTGTGAAAGAAATGGGTCCAGTACTAGTCTTTGAAAAGGGTCAGTC  
TG TAGCTCTTCTTAATGAGAATAGGCAGCTTTTCAGTTGCTCAGGGTCAGATTTCCCTTAGTGGTGTATCTAAT  
CACAGGAAACATCTGTGGTTCCCTCCAGTCTCTTTCTGGGGGACTTGGGCCCACTTCTCATTTCATTTAATT  
AGAGGAAATAGAACTCAAAGTACAATTTACTGTTGTTTAAACAATGCCACAAAGACATGGTTGGGAGCTATTT  
CTTGATTTGTGTAATAATGCTGTTTTGTGTGCTCATAATGGTTCCAAAATTGGGTGCTGGCCAAAGAGAGA  
TACTGTTACAGAAGCCAGCAAGAAGACCTCTGTTTCATTACACCCCCGGGGATATCAGGAATTGACTCCAG  
TGTGTGCAAATCCAGTTTGGCCTATCTTCT

**13712.1&2**

TGAGGGACTGATTGGTTTGCTCTCTGCTATTCAATTCCCCAAGCCCACTTGTTCCCTGCAGCGTCCTCCTTCT  
CATTCCCTTTAGTTGTACCCCTCTCTTTTCATCTGAGACCTTTCCCTTCTTGATGTGCGCTTTTCTTCTTCTTGCTT  
TTTCTGATGTTCTGCTCAGCATGTTCTGGGTGCTTCTCATCTGCATCATTCCCTTTCAGATGCTGTAGCTTCTT  
CCTCCTCTTTCTGCCTCCTTTTCTTTTTCTTTTTTTTTGGGGGGCTTGCTCTCTGACTGCAGTTGAGGGGCCC  
CAGGGTCCTGGCCTTTGAGACGAGCCAGGAAGGCCTGCTCCTGGGCCTCTAGGCGAGCAAGCTTGGCCTT  
CATTGTGATCCCAAGACGGGCAGCCTTGTTGTGCTGTTGCGCCCTCACAGGCTTGGAGCAGCATCTCATCAG  
TCAGAATCTTTGGGGACTTGGACCCCTGGTTGTCGTCATCACTGCAGCTCTCCAAGTCTTTGTTTGGCTTCT  
CTCCACCTGAAGTCAATGTAGCCATCTTCACAACTTCTGATACAGCAAGTTGGGCTTGGGATGATTATAAC  
GGGTGGTCTCCTTAGAAAGGCTCCTTATCTGTACTCCATCCTGCCAGTTTCCACTACCAAGTTGGCCGCA  
GTCTTGTTGAAGAGCTCATTCCACCAGTGGTTTGTGAATCCTTGGCAGGGTCATGTCCTACCCCATGAGT  
GTCTTGCTTCAGYGTACCCCTGAGAGCCTGAGTGATACCATTCTCCTTCCG

**13714.1&2**

GACAACATGAAATAAATCCTAGAGGACAAAATTAACCTCAATAGAGTGAGTCTAGTTAAAACTCGAAAAAT  
GAGCAAGTCTGGTGGGAGTGGAGGAAGGGCTATACTATAAATCCAAGTGGGCCTCCTGATCTTAACAAGCC  
ATGCTCATTATACACATCTCTGAAGTGGACATACCACCTTTACGCAGGAAACAGGGCTTGGAACTTCTAAGG  
GAAATTAACATGCACCACCCACATCTAACCTACCTGCCGGGTAGGTACCATCCCTGCTTCGCTGAAATCAG  
TGCTC

**13716.1&2**

TTGGAATTAATAAACCTGGAACAGGGAAGGTGAAAGTTGGAGTGAGATGTCTTCCATATCTATACCTTTGT  
GCACAGTTGAATGGGAAGTGTGGGTTAGGGCATCTTAGAGTTGATTGATGGAAAAAGCAGACAGGAAC  
TGGTGGGAGGTCAAGTGGGGAAGTTGGTGAATGTGGAATAACTTACCTTTGTGCTCCACTTAACCAGATG  
TGTTGCAGCTTTCCTGACATGCAAGGATCTACTTTAATTCACACTCTCATTAAATAAATTGAATAAAAGGGAA  
TGTTTTGGCACCTGATATAATCTGCCAGGCTATGTGACAGTAGGAAGGAATGGTTCCCTAACAAGCCCAA  
TGCACTGGTCTGACTTTATAAATTATTTAATAAAATGAATATTATC

**13718.2**

AAACTGGACCTGCAACAGGGACATGAATTTACTGCARGGTCTGAGCAAGCTCAGCCCCTCTACCTCAGGGC  
CCCACAGCCATGACTACCTCCCCAGGAGCGGGAGGGTGAAGGGGGCCTGTCTCTGCAAGTGGAGCCAG  
AGTGGAGGAATGAGCTCTGAAGACACAGCACCCAGCCTTCTCGCACCAGCCAAGCCTTAAGTGCCTGCCT  
GACCCTGAACCAGAACCCAGCTGAACTGCCCCCTCCAAGGGACAGGAAGGCTGGGGGAGGGAGTTTACAA  
CCCAAGCCATTCCACCCCCTCCCCTGCTGGGGAGAATGACACATCAAGCTGCTAACAATTGGGGGAAGGG  
GAAGGAAGAAAACCTCTGAAAACAAAATCTTGT

**13722.3**

CATGCGTTTCACCACTGTTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGCAATCCACCCGCCTCAGCCT  
CCAAAAGTGCTGGGATTACAGATGTGAGCCATGGCACCATGCCAAAAGGCTATATTCCTGGCTCTGTGTTT  
CCGAGACTGCTTTTAATCCCAACTTCTCTACATTTAGATTAAAAATATTTTATTCATGGTCAATCTGGAACAT  
AATTACTGCATCTTAAGTTTCCACTGATGTATATAGAAGGCTAAAGGCACAATTTTTATCAAATCTAGTAGAG  
TAACCAAACATAAAATCATTAACTTTCAACTTAATACTAATTGACATTCCTCAAAAGAGCTGTTTTCAAT  
CCTGATAGTTCTTTATTTTTTCAAAATATATTTGCCATGGGATGCTAATTTGCAATAAGGCGCATAATGAGA  
ATACCCCAAACCTGGA

**13722.4**

GTTGGACCCCCAGGGACTGGAAAGACACTTCTTGCCCGAGCTGTGGCGGGAGAAGCTGATGTTCCTTTTTA  
TTATGCTTCTGGATCCGAATTTGATGAGATGTTTGTGGGTGTGGGAGCCAGCCGTATCAGAAATCTTTTTAG  
GGAAGCAAAGGCGAATGCTCCTTGTGTTATATTTATTGATGAATTAGATTCTGTTGGTGGGAAGAGAATTGA  
ATCTCCAATGCATCCATATTCAAGGCAGACCATAAATCAACTTCTTGCTGAAATGGATGGTTTTAAACCCAAT  
GAAGGAGTTATCATAATAGGAGCCACAACTTCCCAGAGGCATTAGATAATGCCTTAATACCGTCCTGGTCG  
TTTTGACATGCAAGTTACAGTTCCAAGGCCAGATGTAAAAGGTGCAACAGAAATTTTGAATGGTATCTCAA  
TAAATAAAGTTTGATCAATCCCGTTGATCCAGAAATTATAGCCTCGAGGTAAGTGGTGGCTTTTCCGGAAGC  
AGAGTTGGGAGAATCTT

**13724-13698-13748**

GCCTACAACATCCAGAAAGAGTCTACCCTGCACCTGGTGTCTSCGTCTCAGAGGTGGGATGCAGATCTTCGT  
GAAGACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCGAGTGACACCATYGAGAACGTCAAAGCA  
AAGATCCARGACAAGGAAGGCRTYCCTCCTGACCAGCAGAGGTTGATCTTTGCCGGAAAGCAGCTGGAAG  
ATGGDCGCACCCTGTCTGACTACAACATCCAGAAAGAGTCYACCCTGCACCTGGTGCTCCGTCTCAGAGGT  
GGGATGCARATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCCAGTGACACCA  
TCGAGAATGTCAAGGCAAAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCT  
GGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACTTGGT  
CCTGCGCTTGAGGGGGGTGTCTAAGTTTCCCCTTTTAAGGTTTCMACAAATTCATTGCACTTTCCTTTCA  
ATAAAGTTGTTGCATTCCC

**13730.1**

GAAGTGGGCCCCTGAGCCCAAGTCATGCCTTGTGTCCGCATCTGCCGTGTACCTCTGTCCTGCCCTCAC  
CCCTCCCTCCTGGTCTTCTGAGCCAGCACCATCTCCAAATAGCCTATTCCTTCCTGCAAATCACACACACAT  
GCGGGCCACACATACCTGCTGCCCTGGAGATGGGGAAGTAGGAGAGATGAATAGAGGCCCATACATTGTA  
CAGAAGGAGGGGGCAGGTGCAGATAAAAGCAGCAGACCCAGCGGCAGCTGAGGTGCATGGAGCACGGTTG  
GGGCCGGCATTGGGCTGAGCACCTGATGGGCCTCATCTCGTGAATCCTCGAGGCAGCGCCACAGCAGAG  
GAGTTAAGTGGCACCTGGGCCGAGCAGAGCAGGAGACTGAGGGTCAGAGTGGAGGCTAAGCTGCCCTGG  
AACTCCTCAATCTTGCCTGCCCCCTAGTATGAAGCCCCCTTCCTGCCCTACAATTCCTGA

**13732.1**

ATGGATCTTACTTTGCCACCCAGGTTGGAGTGCAGTGCTGCAATCTTGGCTCACTGCAGCCTTAACCTCCC  
AGGCTCAAGCTATCCTCCTGCCAAAGCCTTCACATAGCTGGGACTACAGGTACACNGCCACCACACCCAG  
CTAAAATTTTTGTATTTTTGTAGAGACGGGATCTCGCCACGTTGCCCAGGCTGGTCCCATCCTGACCTCAA  
GCAGATCTGCCACCTCAGCCCCCAACGTGCTAGGATTACAGGCGTGAGCCACCGCACCCAGCCTTTGT  
TTTGCTTTTAATGGAATCACCAGTTCCCTCCGTGTCTCAGCAGCAGCTGTGAGAAATGCTTTGCATCTGTG  
ACCTTTATGAAGGGGAACCTCCATGCTGAATGAGGGTAGGATTACATGCTCCTGTTTCCCGGGGGTCAAGA  
AAGCCTCAGACTCCAGCATGATAAGCAGGGTGAG

**13732.2**

ATAGGGGCTTTAAGGAGGGAATTCAGGTTCAATGAGGTCGTAAGGCCAGGGCTCTTATCCAGTAAGACTGG  
GGTCCTTAGATGAGAAAGAGACACCCGAGGTCTTCTCTCTGCCGTGTGAGGATGCATCAAGAAGGCGGC  
CGTCTGCAAGCGAAGGAGAGGGCCGCACCAGAAACCGACACCTTCATCTTGGACTTGCAGCCTCTAGAACT  
GAGAAAATAACTGTCTGTTGGTTAAGCCACCCAGTTTGTAGTATTCTTATGGCTTCCTAAGCAGACTAAC  
AAACAAACACCCAAAATTAAGTATGGCTTCGCTGTCTTCTGTAAAAATTGCTATGAGAGAACTTTTCACTCA  
CTGTTTTGCAGTTTCTCCCTCAGTCCCTGGTTCTTCTTCTCACATAATCCCAATTTCAATTTATAGTTCATGG  
CCCAGGCAGAGTCATTCATCACGGCATCTCCTGAGCTAAACCAGCACCTGCTCTGCTCACTTCTTGACTGG  
CTGCTCATCATCAGCCCTCTTGCAGAGATTTCAATTCCTCCCGTGCCAGGTACTTCACGCACCAAGCTCA

**"REPLACEMENT SHEETS"**

**13735.1**

GGATAATGAAGTTGTTTTATTTAGCTTGGACAAAAAGGCATATTCCTCTATTTTCTTATACAACAAATATCCCC  
AAAATAAAGCAAGCATATATATCTTGAATGTGTAATAATCCAGTGATAAACAAGAGCAGTACTTTAAAAGAAA  
AAAAAATATGTATTTCTGTCAGGTAAAATGAGAATCAAAACCATTTACTCTGCTAACTCATTATTTTTTGCTT  
TCTTTTTGGTTAAGAGAGGCAATGCAATACACTGAAAAAGGTTTTATCTTATCTGGCATTGGAATTAGACAT  
ATTCAAACCCCAGCCCCCATTTCCAACTTTAAGACCACAAACAAGTAATTTACTTTTCTGAACATTGGTTTT  
TTCTGGAATAATGGAATTATAAAATAGACTTTGCAGACTCTTATGAGATTAAATAAGATAATGTATGAAATTCT  
TTCTTCTTTTTTACTTCTTTTTCTTTTTGAGATGGAGTCTCACCCCGTCACCCAGGCTGGAGTACAGTG

**13735.2**

CCACTGCACTCCAGCCTGGGTGACGGAGTGAGACTCTGTCTCAAAAAACAAACAAACAAACAAAA  
ACTGAAAAGGAAATAGAGTTCCTCTTTCCTCATATATGAATATATTATTTCAACAGATTGTTGATCACCTACCA  
TATGCTTGGTATTGTTCTAATTGCTGGGGATACAGCAAGAGGTTCTGCAGAACTTCATGGAGCATGAAAGTA  
AATAAACAAAGTTAATTTCAAGGCCAGGCATGGTTGCTCACACCTTTAGTCCCAGCACTTTGGGAGGCTGA  
GGCAGGTGGATCACTTGGGCCAGGAGTTCAAGGCTGCAGTGAGCCAAGATTGTGCCACTACTCTCCAGG  
CTGGGCAACAGAGCAAGACCCTGTCTCAGGGGAACAAAAAGTTAATTTGAGATTTTGTAAAGTGTGTAA  
GGAAGTAAATAGGTTGATATTCAAGAGAGCACCTGAAGGCCAGGCGTGGTGGCTCACGCCTGTGGTCTAA  
CGCTTTGGGAAGCCCGAGCGGGCGGATCACAAGGTCAGGAGAATTTGGCCAGGCATGGTG

**13736.1**

AGAATCCATTTATTGGGTTTTAACTAGTTACACAACCTGAAATCAGTTTGGCACTACTTTATACAGGGATTAC  
GCCTGTGTATGCCGACACTTAAATACTGTACCAGGACCACTGCTGTGCTTAGGTCTGTATTGAGTCATTGAG  
CATGTAGATACTAAAAATATACTGTAGTGTTCTTTAAGGAAGACTGTACAGGGTGTGTTGCAAGATGACAT  
TCACCAATTTGTGAATTATTTCAACCCAGAAGATACCTTTCACTCTATAAACTTGTGATAGGCCAAACATGTGG  
TGTTAGCATTGAGAGATGCACACAAAAATGTTACATAAAAGTTCAGACATTCTAATGATAAGTGAAGTAAAA  
AAAAAAAAACCCACATCTCAATTTTTGTAACAAGATAAAGAAAATAATTTAAAAACACAAAAAATGGCATTCA  
GTGGGTACAAAGCC

**13737.1&2**

CAAATATTTAATATAAATCTTTGAAACAAGTTCAGAKGAAATAAAAAATCAAAGTTTGCAAAAACGTGAAGATTA  
ACTTAATTGTCAAATATTCCTCATTGCCCCAAATCAGTATTTTTTTTATTTCTATGCAAAAAGTATGCCTTCAA  
CTGCTTAAATGATATATGATATGATACACAAACCAGTTTTCAAATAGTAAAGCCAGTCATCTTGCAATTGTAA  
GAAATAGGTAAAAGATTATAAGACACCTTACACACACACACACACACACACACAGTGTGCACcGCCAAT  
GACAAAAACAATTTGGCCTCTCCTAAAAATAAGAACATGAAGACCCTTAATTGCTGCCAGGAGGGAACACTG  
TGTCACCCCTCCCTACAATCCAGGTAGTTTCCTTTAATCCAATAGCAAATCTGGGCATATTTGAGAGGAGTG  
ATTCTGACAGCCACSGTTGAAATCCTGTGGGGAACCATTCATGTCCACCCACTGGTGCCCTGAAAAAATGC  
CAATAATTTTTCGCTCCCACTTCTGCTGCTGTCTTCCACATCCTCACATAGACCCAGACCCGCTGGCCC  
CTGGCTGGGCATCGCATTGCTGGTAGAGCAAGTCATAGGTCTCGTCTTTGACGTCACAGAAGCGATACACC  
AAATTGCCTGGTCCGTCATTGTCATAACCAG

**"REPLACEMENT SHEETS"**

**13738.1**

TTTGACTTTAGTAGGGGTCTGAACTATTTATTTTACTTTGCCMGTAATATTTARACCYTATATATCTTTTCATTA  
TGCCATCTTATCTTCTAATGBCAAGGGAACAGWTGCTAAMCTGGCTTCTGCATTWATCACATTAATAATGGC  
TTTCTTGAAAAATCTTCTTGATATGAATAAAGGATCTTTTAVAGCCATCATTTAAAGCMGGNTTCTCTCCAAC  
ACGAGTCTGCTSASGGGGGGKGAGCTGTGAACTCTGGCTGAAGGCTTTCCCATACACACTGCAATGACMT  
GGTTTCTGACCAGBGTGAGTTA

**13738.2**

AGAGAAGCCCCATAAATGCAATCAGTGTGGGAAGGCCTTCAGTCAGAGCTCAAGCCTTTTCCTCCATCATC  
GGGTTCATACTGGAGAGAAACCCTATGTATGTAATGAATGCGGCAGAGCCTTTGGTTTTAACTCTCATCTTA  
CTGAACACGTAAGGATTCACACAGGAGAAAAACCCTATGTTTGTAATGAGTGCGGCAAAGCCTTTTCGTCCGG  
AGTTCCACTCTTGTTTCAGCATCGAAGAGTTCACACTGGGGAGAAGCCCTACCAGTGCGTTGAATGTGGGAA  
AGCTTTCAGCCAGAGCTCCAGCTCACCCCTACATCAGCCGAGTTCACACTGGAGAGAAGCCCTATGACTGT  
GGTGAAGTGTGGGAAGGCCTTCAGCCGGAGGTCAACCCTCATTGAGCATCAGAAAGTTCACAGCGGAGAGA  
CTCGTAAGTGCAGAAAACATGGTCCAGCCTTTGTTTCATGGCTCCAGCCTCACAGCAGATGGACAGATTCCC  
ACTGGAGAGAAGCACGGCAGAACCTTTAACCATGGTGCAAATCTCATTCTGCGCTGGACAGTTC

**13739.1&2**

GAGACAGGGTCTCACTTTGTCACCCAGGCTGGAATGCAGTGGTGCGATCTTACGTAGCTCACTGCAGCCCT  
GACCTCCTGGACTCAAACAATTCTCCTGCCTCAGCCCTGCAAGTAGCTGGGACTGTGGGTGCATGCCACCA  
TGCCTGGCTAACTTTTGTAGTTTTTGTAAAGATGGGGTTTTGCCATGTTGCACATGCTGGTCTTGAACCTCT  
GAGCTCAAACGATCTGCCACCTCGGCCTCCAGAAATGTTGGGATTACAGGGGTAAACCACCACGCCTGG  
CCCCATTAGGGTATTCTTAGCATCCACTTGCTCACTGAGATTAATCATAAGAGATGATAAGCACTGGAAGAA  
AAAAATTTTTACTAGGCTTTGGATATTTTTTCTTTTTTCAGCTTTATACAGAGGATTGGATCTTTAGTTTTCT  
TTAACTGATAATAAAACATTGAAAGGAAATAAGTTTACCTGAGATTCACAGAGATAACCGGCATCACTCCCTT  
GCTCAATTCAGTCTTTACCACATCAATTATTTTCAGAGGTGCAGGATAAAGGCCTTTAGTCTGCTTTTCGCA  
CTTTTTCTTCCACTTTTTTGTAAACCTGTTGCCTGACAAATGGAATTGACAGCGTATGCCATGACTATTCCAT  
TTGTCAGGCATACGCTGTCAATTTTTCCACCAATCCCTTGTCTCTCTTTGGAGAGATCTTCTTATCAGCTAGT  
CCTTTGGCAAAGTAATTGCAACTTCTTCTAGGTATTCTATTGTCCGTTCCACTGGTGGAAACCCCTGGGACC  
AGGACTAAAACCTCCAG

**13741.1**

ATCTCATATATATATTTCTTCTGACTTTATTTGCTTGCTTCTGNCACGCATTTAAAAATATCACAGAGACCAAA  
ATAGAGCGGCTTTCTGGTGGAACGCATGGCAGTCACAGGACAAAATACAAAACCTAGGGGGCTCTGTCTTCT  
CATACATCATACAATTTTCAAGTATTTTTTTTATGTACAAAGAGCTACTCTATCTGAAAAAAATTAATAAATAA  
ATGAGACAAAGATAGTTTATGCATCCTAGGAAGAAAGAATGGGAAGAAAGAACGGGGCAGTTGGGTACAGAT  
TCCTGTCCCCTGTTCCAGGGACCACTACCTTCTGCCACTGAGTTCCCCACAGCCTCACCCATCATGTC  
ACAGGGCAAGTGCCAGGGTAGGTGGGGACCACTGGAGACAGGAACCAGCAACATACTTTGGCCTGGAAG  
ATAAGGAGAAAGTCTCAGAAACACACTGGTGGGAAGCAATCCACNGGCCGTGCCCCANGAGCTTCCCAC  
CTGCTGCTGGCTCCCTGGGTGGCTTTGGGAACAGCTTGGGCAGGCCCTTTTGGGTGGGGNCCAACCTGGG  
CCTTTGGGCCCGTGTGGAAAG

13742.1

AAACATTGAGATGGAATGATAGGGTTTCCCAGAATCAGGTCCATATTTTAACTAAATGAAAATTATGATTTAT  
AGCCTTCTCAAATACCTGCCATACTTGATATCTCAACCAGAGCTAATTTTACCTCTTTACAAATTAATAAGC  
AAGTAACTGGATCCACAATTTATAATACCTGTCAATTTTTCTGTATTAAACCTCTATCATAGTTTAAGCCTAT  
TAGGGTACTTAATCCTTACAAATAAACAGGTTTAAAATCACCTCAATAGGCAACTGCCCTTCTGGTTTTCTTC  
TTGACTAAACAATCTGAATGCTTAAGATTTTCCACTTTGGGTGCTAGCAGTACACAGTGTTACACTCTGTAT  
TCCAGACTTCTTAAATTATAGAAAAAGGAATGTACACTTTTTGTATTCTTTCTGAGCAGGGCCGGGAGGCAA  
CATCATCTACCATGGTAGGGACTTGTATGCATGGACTACTTTA

14351.1

ACTCTGTGCCCCAGGCTGGAGCCCBTGGMGCGATCTCGACTCCCTGCAAGCTMCGCCTCACAGGWTC  
TGCCATTCTCCTGCCTCAGCATCTGGAGTAGCTGGGACTACAGGCGCCAGCCACCATGCCAGCTAATTTT  
T

14351.2

ACCTTAAAGACATAGGAGAATTTATACTGGGAGAGAAAGCTTACAAATGTAAGGTTTCTGACAAGACTTGGG  
AGTGATTCACACCTGGAACAACATACTGGACTTCACACTGGABAGAAACCTTACAAGTGTAATGAGTGTGGC  
AAAGCCTTTGGCAAGCAGTCAACACTTATTCACCATCAGGCAATTCA

14354.2

AGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGGAGGGCCAAATATGTGGGCTATTACATCTG  
AAGAACGTAATAAGCATGATAAACAGTTTGATAACCTCAAACCTTCAGGAGGTTACATAACAGGTGATCAAG  
CCCGTACTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTTAGCTGAAATATGGGCCTTATCAGATCTGA  
ACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTATGAACTCATCAAGTTAAAGTTGCAGGGC  
CAACAGCTGCCTGTAGTCTCCTCCTATCATGAAACAACCCCTATGTTCTCTCCACTAATCTCTGCTCGT  
TTTGGGATGGGAAGCATGCCAATCTGTCCATTCATCAGCCATTGCCTCCAGTTGCACCTATAGCAACACC  
CTTGTCTTCTGCTACTTCAGGGACCAGTATTCCTCCCTAATGATGCCTGCT

14354.1

CTTTCGATTTCTTCAATTTGTCACGTTTGATTTTATGAAGTTGTTCAAGGGCTAACTGCTGTGTATTATAGCT  
TTCTCTGAGTTCCTTCAGCTGATTGTTAAATGAATCCATTTCTGAGAGCTTAGATGCAGTTTCTTTTTCAAGA  
GCATCTAATTGTTCTTTAAGTCTTTGGCATAATTCTTCTTTCTGATGACTTTCTATGAAGTAACTGATCCC  
TGAATCAGGTGTGTTACTGAGCTGCATGTTTTAATTCTTTCTGTTAATAGCTGCTTCTCAGGGACCAGATAG  
ATAAGCTTATTTTGATATTCCTTAAGCTCTTGGTGAAGTTGTTGATTTCATAATTTCCAGGTCACACTGGT  
TATCCCAAACCTCT



**16431.1.2**

TGGAGGTGAAACGGAGGCAAGAAAGGGGGCTACCTCAGGAGCGAGGGACAAAGGGGGCGTGAGGCACC  
TAGGCCGCGGCACCCCGGCGACAGGAAGCCGTCTGAACCGGGCTACCGGGTAGGGGAAGGGCCCGCG  
TAGTCCTCGCAGGGCCCCAGAGCTGGAGTCGGCTCCACAGCCCCGGGCCGTGGCTTCTCACTTCCTGG  
ACCTCCCCGGCGCCCGGGCCTGAGGACTGGCTCGGCGGAGGGAGAAGAGGAAACAGACTTGAGCAGCTC  
CCCGTTGTCTCGCAACTCCACTGCCGAGGAACCTCTCATTTCTTCCCTCGCTCCTTACCCCCACCTCATGT  
AGAAAGGTGCTGAAGCGTCCGGAGGGAAGAAGAACCTGGGCTACCGTCCTGGCCTTCCCMCCCCCTTCC  
CGGGGCGCTTTGGTGGGCGTGAGTTGGGGTTGGGGGGGTGGGTGGGGTTCTTTTTTGGAGTGCTGGG  
GAACTTTTTTCCCTTCTTCAGGTCAGGGGAAAGGGAATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGA  
CGGGAGTGAGGAGCTTCTGGAACTTTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCG  
TCACCGCTTGGTATCGAAGCACAAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCC  
GAAGCAGCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCCGACAC  
CTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGTGGATCAGATCGGAGC  
GACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGGGACTTACTAAAAGCTAAACAGACCG

**16432-1**

GACATGTTTGCCTGCAGGGGACCAGAGACAATGGGATTAGCCAGTGCTCACTGTTCTTTATGCTTCCAGAG  
AGGATGGGGACAGCTCTCAGGTCAGAATCCAGGCTGAGAAGGCCATGCTGGTTGGGGGCCCCCGGAAGC  
ACGGTCCGGATCCTCCCTGGCATCAGCGTAGACCCGCTGCTCAGGCTTGGGGTACCAAACCTCATGCTCTG  
TACTGTTTTGGCCCCATGCGGTGAGAGGAAAACCTAGAAAAAGATTGGTCGTGCTAAGGAATCAGCTGCCC  
CCTCATCCTCCGCATCCAATGCTGGTGACAACATATTCCCTCTCCAGGACACAGACTCGGTGACTCCACA  
CTGGGCTGAGTGGCCTCTGGAGGCTCGTGGCCTAAGGCAGGGCTCCGTAAGGCTGATCGGCTGAACTGG  
GTGGGGTGAGGGTTTCTGACCCTTCGCTTCCCATCCATAACCGCTGTCAATGAGCTCACACTGTGGTCA

**16432-2**

GATGGCATGGTCGTTGCTAATGTGCCTGCTGGGATGGAGCACTTCCTCCTGTGAGCCAGGGGACCCGCC  
TGTCCCTGGAGCTTGGGGCAAGGAGGGAAGAGTGATACCAGGAAGGTGGGGCTGCAGCCAGGGGGCCAGA  
GTCAGTTCAGGGAGTGGTCCTCGGCCCTCAAAGCTCCTCCGGGGACTGCTCAGGAGTGATGGTGCCCTGG  
AGTTTGCCCCAAGTTCCCTGGCCACCCTGGAAGGTGCCTGGCTGCTCCAGGCCTCTAGGCTGGGCTGATG  
GGTTTCTCCAGGACACAAGTATCATTAAAGCCACCCTCTCCTCAGCTTGTGAGGCCGCACATGTGGGACAG  
GCTGTGCTCACAACCCCTCGCCTGCCCTGCCCTCCATCAGGAGGAGCCAGTGGAAACCTTCGGAAAGCTC  
CCAGCATCTCAGCAGCCCTCAAAGTCGTCTGGGGCAAGCTCTGGTTCTCCTGACTGGAGGTATCTGG  
GCTTGGCCTGCTCTCTCTCGC

**17184.3**

TAAAAAGTGTAACAAAGGTTTATTTAGACTTTCTTCATGCCCCAGATCCAGGATGTCTATGTAAACCGTTA  
TCTTACAAAGAAAGCACAAATATTTGGTATAAACTAAGTCAGTGACTTGCTTAACTGAAATAGCGTCCATCCAA  
AAGTGGGTTTAAAGTAAACTACCTGACGATATTGGCGGGGATCCTGCAGTTTGGACTGCTTGCCGGGTTT  
GTCCAGGGTTCCGGGTCTGTTCTTGGCACTCATGGGGACAGGCATCCTGCTCGTCTGTGGGGCCCCGCTG  
GAGCCCTTACGTGAAGCTGAAGGTATCGACCSTAGGGGGCTCTAGGGCAGTGGGACCTTCATCCGGAACT  
AACAAAGGTCGGGGAGAGGCCTCTTGGGCTATGTGGG

17184.4

CAAGCGTTCCTTTATGGATGTAAATTCAAACAGTCATGCTGAGCCATCCCGGGCTGACAGTCACGTTWAAG  
ACACTAGGTCGGGCGCCACAGTGCCACCCAAGGAGAAGAAGAAATTTGGAATTTTCCATGAAGATGTACGG  
AAATCTGATGTTGAATATGAAAATGGCCCCCAAATGGAATTCAAAAGGTTACCACAGGGGCTGTAAGACCT  
AGTGACCCTCCTAAGTGGGAAAGAGGAATGGAGAATAGTATTTCTGATGCATCAAGAACATCAGAATATAAA  
ACTGAGATCATAATGAAGGAAAATTCCATATCCAATATGAGTTTACTCAGAGACAGTAGAAACTATTCCCAG  
G

17185.1

TAGGAATAACAAATGTTTATTCAGAAATGGATAAGTAATACATAATCACCTTCATCTCTTAATGCCCCTTCC  
TCTCCTTCTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGGAGGAGGACACAGGACTAG  
CCCACCACCTTCTCTTCCCGGTCTCCCAAGATGACTGCTTATAGAGTGGAGGAGGCAAACAGGTCCCCTCA  
ATGTACCAGATGGTCACCTATAGCACCAGCTCCAGATGGCCACGTGGTTGCAGCTGGACTCAATGAAACTC  
TGTGACAACCAGAAGATACCTGCTTTGGGATGAGAGGGAGGATAAAGCCATGCAGGGAGGATATTTACCAT  
CCCTACCCTAAGCACAGTGCAAGCAGTGAGCCCCCGGCTCCAGTACCTGAAAAACCAAGGCCTACTGNC  
TTTTGGATGCTCTCTTGGGCCACG

17188.2

AAGCCTCCTGCCCTGGAAATCTGGAGCCCCTTGGAGCTGAGCTGGACGGGGCAGGGAGGGGCTGAGAGG  
CAAGACCGTCTCCCTCCTGCTGCAGCTGCTTCCCAGCAGCCACTGCTGGGCACAGCAGAAACGCCAGCA  
GAGAAAATGGGAGCCGAGAGTCCTTAGCCCTGGAGCTGAGGCTGCCTCTGGGCTGACCCGCTGGCTGTA  
CGTGGCCAGAACTGGGGTTGGCATCTGGCATCCATTTGAGGCCAGGGTGGAGGAAAGGGAGGCCAACAG  
AGGAAAACCTATTCTGCTGTGACAACACAGCCCTTGTCCACGCAGCCTAAGTGCAGGGAGCGTGATGAA  
GTCAGGCAGCCAGTCGGGGAGGACGAGGTAAGTACAGCAGCAATGTCACCTTGTAGCCTATGCGCTCAATG  
GCCCGGAGGGGCAGCAACCCCCCGCACACGTCAGCCAACAGCAGTGCCTCTGCAGGCACCAAGAGAGCG  
ATGATGGACTTGAGCGCCGTGTTT

17190.1

GTTTGGCAGAAGACATGTTTAATAACATTTTCATATTTAAAAAATACAGCAACAATTCTCTATCTGTCCACCAT  
CTTGCCTTGCCCTTCCTGGGGCTGAGGCAGACAAAGGAAAGGTAATGAGGTTAGGGCCCCCAGGCGGGCT  
AAGTGCTATTGGCCTGCTCCTGCTCAAAGAGAGCCATAGCCAGCTGGGCACGGCCCCCTAGCCCCTCCAG  
GTTGCTGAGGCGGCAGCGGTGGTAGAGTTCTTCACTGAGCCGTGGGCTGCAGTCTCGCAGGGAGAACTTC  
TGCACCAGCCCTGGCTCTACGGCCCGAAAGAGGTGGAGCCCTGAGAACCGGAGGAAAACATCCATCACCT  
CCAGCCCCTCCAGGGCTTCCTCCTCTTCTGGCCTGCCAGTTCACCTGCCAGCCGGGCTCGGGCCGCCA  
GGTAGTCAGCGTTGTAGAAGCAGCCCTCCGCAGAAGCCTGCCGGTCAAATCTCCCCGCTATAGGAGCCCC  
CCGGGAGGGGTGAGCACC

17190.2

CAAGTTGAACGTCAGGCTTGGCAGAGGTGGAGTGTAGATGAAAACAAAGGTGTGATTATGAAGAGGATGTG  
AGTCCTTTGGGTGTAGGAGAGAAAGGCTGTTGAGCTTCTATTTCAAGATACTTTTACCTGTGCAAAAAGCAC  
ATTTCCACCTCCTTCTCATGGCATTGTGTAAAGGTGAGTATGATTCCATTCCATCTGCATTTTAGAGGTGA  
AGAATAACGTACAAGGGATTCAAGTATTAGCAAGGGACCCCTCACTAAGTGTGATGGAGTTAGGACAGAG  
CTCAGCTGTTTGAATCTCAGAGCCCAGGCAGCTGGAGCTGGGTAGGATCCTGGAGCTGGCACTAATGTGA  
GGTGCATTCCCTCCAACCCAGGCTCAGATCCGGAACCTGACCGTGCTGACCCCGAAGGGGAGGCAGGG  
CTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCACACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACT  
ACTTCACAGAGCAGC

17191.2&89.2

TGGCCTGGGCAGGATTGGGAGAGAGGTAGCTACCCGGATGCAGTCCTTTGGGATGAAGACTATAGGGTAT  
GACCCCATCATTTCCCAGAGGTCTCGGCCTCCTTTGGTGTTCAGCAGCTGCCCCTGGAGGAGATCTGGC  
CTCTCTGTGATTTCACTACTGTGCACACTCCTCTCCTGCCCTCCACGACAGGCTTGCTGAATGACAACACCT  
TTGCCAGTGCAAGAAGGGGGTGCCTGTGGTGAAGTGTGCCCCTGGAGGGATCGTGGACGAAGGCGCCC  
TGCTCCGGGGCCCTGCAGTCTGGCCAGTGTGCCGGGGCTGCACTGGACGTGTTTACGGAAGAGCCGCCAC  
GGGACCGGGCCCTTGGTGGACCATGAGAATGTCATCAGCTGTCCACCTGGGTGCCAGCACCAAGGAGG  
CTCAGAGCCGCTGTGGGGAGGAAATTGCTGTTCAAGTTCGTGGACATGGTGAAGGGGAAATCTCTCACGGG  
GGTTGTGAATGCCAGGCCCTT

**"REPLACEMENT SHEETS"**

AGCCAGATGGCTGAGAGCTGCAAGAAGAAGTCAGGATCATGATGGCTCAGTTTCCCACAGCGATGAATGG  
AGGGCCAAATATGTGGGCTATTACATCTGAAGAACGTACTAAGCATGATAAACAGTTTGATAACCTCAAACC  
TTCAGGAGGTTACATAACAGGTGATCAAGCCCGTACTTTTTTCTACAGTCAGGTCTGCCGGCCCCGGTTTT  
AGCTGAAATATGGGCCTTATCAGATCTGAACAAGGATGGGAAGATGGACCAGCAAGAGTTCTCTATAGCTA  
TGAAACTCATCAAGTTAAAGTTGCAGGGCCAACAGCTGCCTGTAGTCCTCCCTCCTATCATGAAACAACCCC  
CTATGTTCTCTCCACTAATCTCTGCTCGTTTTTGGGATGGGAAGCATGCCCAATCTGTCCATTCATCAGCCAT  
TGCTCCAGTTGCACCTATAGCAACACCCTTGCTTCTGCTACTTCAGGGACCAGTATTCCTCCCCTAATGA  
TGCTGCTCCCCTAGTGCCTTCTGTTAGTACATCCTCATTACCAAATGGAAGTCCAGTCTCATTGAGCCTT  
TATCCATTCTTATTCTTCTTCAACATTGCCTCATGCATCATCTTACAGCCTGATGATGGGAGGATTTGGTGG  
TGCTAGTATCCAGAAGGCCAGTCTCTGATTGATTTAGGATCTAGTAGCTCAACTTCCTCAACTGCTTCCCT  
CTCAGGGAAGTCACTAAGACAGGGACCTCAGAGTGGGCAGTTCCTCAGCCTTCAAGATTAAAGTATCGGC  
AAAAATTTAATAGTCTAGACAAAGGCATGAGCGGATACCTCTCAGGTTTTCAAGCTAGAAATGCCCTTCTTC  
AGTCAAACTCTCTCAAACTCAGCTAGCTACTATTTGGACTCTGGCTGACATCGATGGTGACGGACAGTTGA  
AAGCTGAAGAATTTATTCTGGCGATGCACCTCACTGACATGGCCAAAGCTGGACAGCCACTACCACTGACG  
TTGCCTCCCGAGCTTGCTCCCTCCATCTTTCAGAGGGGGAAAGCAAGTTGATTCTGTTAATGGAAGTCTGCCT  
TCATATCAGAAAACACAAGAAGAAGAGCCTCAGAAGAACTGCCAGTTACTTTTGAGGACAAACGGAAAGC  
CAACTATGAACGAGGAAACATGGAGCTGGAGAAGCGACGCCAAGTGTGATGGAGCAGCAGCAGAGGGA  
GGCTGAACGCAAAGCCCAGAAAGAGAAGGAAGAGTGGGAGCGGAAACAGAGAGAACTGCAAGAGCAAGA  
ATGGAAGAAGCAGCTGGAGTTGGAGAAACGCTTGGAGAAACAGAGAGAGCTGGAGAGACAGCGGGAGGA  
AGAGAGGAGAAAGGAGATAGAAAGACGAGAGGCAGCAAAACAGGAGCTTGAGAGACAACGCCGTTTAGAA  
TGGGAAAGACTCCGTCGGCAGGAGCTGCTCAGTCAGAAGACCAGGGAACAAGAAGACATTGTCAGGCTGA  
GCTCCAGAAAGAAAAGTCTCCACCTGGAAGTGGAAAGCAGTGAATGGAAAACATCAGCAGATCTCAGGCAGA  
CTACAAGATGTCCAAATCAGAAAGCAAACACAAAAGACTGAGCTAGAAGTTTTGGATAAACAGTGTGACCTG  
GAAATTATGGAAATCAAACAACCTTCAACAAGAGCTTAAGGAATATCAAATAAGCTTATCTATCTGGTCCCTG  
AGAAGCAGCTATTAAACGAAAGAATTAACAAACATGCAGCTCAGTAACACACCTGATTCAGGGATCAGTTTAC  
TTCATAAAAAGTCATCAGAAAAGGAAGAATTATGCCAAAGACTTAAAGAACAATTAGATGCTCTTGAAAAAGA  
AACTGCATCTAAGCTCTCAGAAATGGATTCATTTAACAATCAGCTGAAGGAACTCAGAGAAAGCTATAATAC  
ACAGCAGTTAGCCCTTGAACAACCTCATAAAATCAAACGTGACAAATTGAAGGAAATCGAAAGAAAAAGATT  
AGAGCAAAAAAAAAAAAAA

**"REPLACEMENT SHEETS"**

ATGGCAGTGACATTCACCATCATGGGAACCACTTCCCTTTTCTTCAGGATTCTCTGTAGTGGAAGAGAGCA  
CCCAGTGTTGGGCTGAAAACATCTGAAAGTAGGGAGAAGAACCTAAAATAATCAGTATCTCAGAGGGCTCT  
AAGGTGCCAAGAAGTCTCACTGGACATTTAAGTGCCAACAAAGGCATACTTTCGGAATCGCCAAGTCAAAA  
CTTTCTAACTTCTGTCTCTCTCAGAGACAAGTGAGACTCAAGAGTCTACTGCTTTAGTGGCAACTACAGAAA  
ACTGGTGTTACCCAGAAAAACAGGAGCAATTAGAAATGGTTCCAATATTTCAAAGCTCCGCAAACAGGATGT  
GCTTTCCTTTGCCCATTTAGGGTTTCTTCTCTTTCCTTTCTCTTTATTAACCACTA

*Fig. 2B*

ATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATA  
TGAACAAGATAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAAATAATTCATGTGAAGTAGACAAGTGTG  
TTAAGAGTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTATGTTATATGTGCTGTAATG  
TTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCACAAATTAAGCTGTAG  
TATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAGTAATGGGT  
CAAATGATTCACCTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTG  
AGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGCGACACCGATTTTATAAATAAACTGAGCACCTT  
CTTTTAAACAAACAAATGCGGGTTTATTTCTCAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTT  
TCACCTTGACTATATGGCATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTA  
AGACCTCAGTTTTCAATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCCCCCATCTCCGGGG  
GAATGTCTGAAGACAATTTTGTTACCTCAATGAGGGAGTGGAGGAGGATACAGTGCTACTACCAACTAGTG  
GATAAAGGCCAGGGATGCTGCTCAACCTCCTACCATGTACAGGACGTCTCCCCATTACAACCTACCCAATCC  
GAAGTGTCAACTGTGTCAGGACTAAGAAACCCTGGTTTTGAGTAGAAAAGGGCCTGGAAAGAGGGGAGCC  
AACAAATCTGTCTGCTTCCTCACATTAGTCATTGGCAAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGC  
ACAGAGAGCCAGAACTCTATCGGGCACCAGGATAACATCTCTCAGTGAACAGAGTTGACAAGGCCTATGGG  
AAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTCTAAGTTTCTTTCCCTTCATTCTACCCTGCAAGCCA  
AGTTCTGTAAGAGAAATGCCTGAGTTCTAGCTCAGGTTTTCTACTCTGAATTTAGATCTCCAGACCCTTCCT  
GGCCACAATTCAAATTAAGGCAACAAACATATACCTTCCATGAAGCACACACAGACTTTTGAAAGCAAGGAC  
AATGACTGCTTGAATTGAGGCCTTGAGGAATGAAGCTTTGAAGGAAAAGAATACTTTGTTTCCAGCCCCCTT  
CCCACACTCTTCATGTGTTAACCCTGCCTTCCTGGACCTTGAGCCACGGTGACTGTATTACATGTTGTTA  
TAGAAAATGATTTTAGAGTTCTGATCGTTCAAGAGAATGATTAAATATACATTTCTTA

Element Display											
Diff Exp	Probe1	Exp	Probe2	GEM/Element	Plate/Well	Probe1	S/B	A%	Probe2	S/B	A%
+1.7	384A Ovary T (nets)		272A Dendritic cells	422A0608 (420)	421G0196 (C:11)	2393	13.7	50	1430	2.0	50
-1.1	335A Ovary T		S7 Ovary N	422D0626 (420)	421G0196 (C:11)	355	2.7	54	382	1.8	54
+1.8	261A Ovary T		S10 Skeletal muscle N	42230621 (420)	421G0196 (C:11)	1298	6.9	51	707	1.9	51
+8.1	264A Ovary T		S2 Pancreas N	422N0629 (420)	421G0196 (C:11)	9590	44.1	62	1190	2.3	62
-1.2	386A Ovary T		S40 PBMC (activated)	422J0605 (420)	421G0196 (C:11)	516	3.8	50	618	2.0	50
+4.7	265A Ovary T		CT5 Heart N	422Q0624 (420)	421G0196 (C:11)	2305	14.1	53	489	2.2	53
-1.4	S25 Ovary T		CT4 Bone Marrow N	422H0619 (420)	421G0196 (C:11)	531	3.5	53	743	2.0	53
	383A Ovary T (nets)		I1 Colon N	422B0609 (420)	421G0196 (C:11)	1842	10.1	39	671	2.0	39
-1.9	S22 Ovary T		CT9 Kidney N	42290627 (420)	421G0196 (C:11)	453	3.3	66	657	3.2	66
+3.2	9485 OT 1-P (SCID)		9485 OT 5-P (SCID)	422Y0602 (420)	421G0196 (C:11)	1882	12.1	57	594	2.3	57
+1.5	262A Ovary T		334A Large Intestine N	422A0622 (420)	421G0196 (C:11)	1486	7.5	55	965	2.2	55
-1.1	S115 Ovary T (nets)		CT10 Small Intestine N	422C0604 (420)	421G0196 (C:11)	509	3.4	51	573	2.0	51
+1.1	288A Ovary T		CT12 Lung N	422V0625 (420)	421G0196 (C:11)	700	4.5	54	651	2.1	54
-2.1	201A Ovary T		S6 Stomach N	422W0620 (420)	421G0196 (C:11)	625	4.6	46	1335	3.6	46
+7.8	S23 Ovary T		S56 Spinal Cord N	422G0628 (420)	421G0196 (C:11)	3896	22.1	50	502	2.2	50
+1.8	205A Ovary T		270A Liver N	422Q0606 (420)	421G0196 (C:11)	2251	14.7	46	1256	2.0	46
-1.9	9334 Ovary T (SCID)		I2 Skin N	422R0601 (420)	421G0196 (C:11)	552	3.4	72	1029	2.3	72
+5.6	385A Ovary T		S91 Fetal tissue	422X0607 (420)	421G0196 (C:11)	8126	35.1	50	1449	2.0	50
-3.5	263A Ovary T		S73 Breast N	422H0623 (420)	421G0196 (C:11)	439	3.2	61	1531	3.4	61
-3.3	382A Ovary T		CT19 Brain N	422Q0610 (420)	421G0196 (C:11)	387	3.2	50	1278	2.1	50
+4.8	266A Ovary T		S27 Ovary N	42250603 (420)	421G0196 (C:11)	4242	22.1	58	883	2.0	58

Fig. 3

Serial No. 09/827,271 Docket No. 210121.462C6

Inventor(s): Jennifer L. Mitcham et al.

Express Mail No. EV719392064US

**"REPLACEMENT SHEETS"**

TCGAGCGGCCGCCCAGGTCCTTCAGACTTGGACTGTGTCACACTGCCAGGCTTCCAGGGCTCCAAC  
TTGCAGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACA  
CCATGGTTTTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTG  
GATATTTCTACCTCGGCCGCGACCACGCT

*Fig. 4*



**"REPLACEMENT SHEETS"**

TAGCGYGGTCGCGGCCGAGGYCTGCTTYTCTGTCCAGCCCAGGGCCTGTGGGGTCAGGGCGGTGGGTGC  
AGATGGCATCCACTCCGGTGGCTTCCCCATCTTTCTCTGGCCTGAGCAAGGTCAGCCTGCAGCCAGAGTA  
CAGAGGGCCAACACTGGTGTCTTGAACAAGGGCCTTAGCAGGCCCTGAAGGRCCCTCTCTGTAGTGTG  
AACTTCCTGGAGCCAGGCCACATGTTCTCCTCATACCGCAGGYTAGYGATGGTGAAGTTGAGGGTGAAATA  
GTATTMANGRAGATGGCTGGCARACCTGCCCCGGCGGCCGCTCSAAATCC

**"REPLACEMENT SHEETS"**

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTCAGCTCT  
CTGTACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTG  
TCTGCACCCATCGTCCTGACCCCAAAGCCCTGGACTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCA  
GCTGACCCACGGCATCACTGAGCTGGGCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTC  
ACCCATCGGAGCTCTGTACCCACCACCAGCACCGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGG  
CGGCCGCTCGA

*Fig. 6*

**Fig. 7A**

TTGGGGNTTTTMGAGCGGCCGCCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTCACTGAACTT  
CACCATCAACAACCTGCGGTATGAGGAGAACATGCAGCACCTGGCTCCAGGAAGTTCAACACCACGGAG  
AGGGTCCTTCAGGGCCTGCTCAGGTCCCTGTTCAAGAGCACCAAGTGTGGCCCTCTGTACTCTGGCTGCA  
GACTGACTTTGCTCAGACTTGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCT  
TGATCCCACTGGTCCTGGACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGTCCTCTGGCGGNGAC  
NCCNCTT

**Fig. 7B**

AGCGTGGTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATC  
TCTGCTGTCAGTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAGTGCATTTAATACACCTAACGTATC  
GAACATCATAGCTTGGCCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCCG  
GGCGGCCGCTCGA

*Fig. 7A and 7B*

**"REPLACEMENT SHEETS"**

TGTGGTGTGAACTTCCTGGAGNCAGGGTGACCCATGTCCTCCCCATACTGCAGGTTGGTGATGGTGAAGT  
TGAGGGTGAATGGTACCAGGAGAGGGCCAGCAGCCATAATTGTSGRGCKGSMGMSSGAGGMWGGWGTY  
YCWGAGGTTTCYRARRTCCACTGTGGAGGTCCCAGGAGTGCTGGTGGTGGGCACAGAGSTCYGATGGGTG  
AAACCATTGACATAGAGACTGTTCTGTCCAGGGTGTAGGGGGCCCAGCTCTTYRATGYCATTGGYCAGTTK  
GCTYAGCTCCCAGTACAGCCRCTCTCKGYGGMWCCAGSGCTTTTGGGGTCAAGATGATGGATGCAGATG  
GCATCCACTCCAGTGGCTGCTCCATCCTTCTCGGACCTGAGAGAGGTCAGTCTGCAGCCAGAGTACAGAG  
GGCCAACACTGGTGTCTTTGAATA

**"REPLACEMENT SHEETS"**

TCGAGCGGCCGCCCCGGGCAGGTCAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGT  
GCTGCGGACATCTCCAGGGAGTGCAGAAGGGAAGCAGGTCAAACCTGCTCAGATCAGTCAGACTGGCTGTT  
CTCAGTTCTCACCTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTTCCTTGAACAA  
GGGCTTGAGCAGACCCTGCAGAACCCTCTTCCGTGGTGTGAACTTCCTGGAAACCAGGGTGTTCATGTT  
TTTCCTCATAATGCAAGGTTGGTGATGG

***Fig. 9***

Gene Name	Bal Probe 1 Exp Name	P1	P2 Name	Probe 2 ID	Probe 1 Value	Probe 2 Value	Probe 1 S/B	Probe 1 A%	Probe 2 S/B	Probe 2 A%
42100188 (D3)	+7.0 205A Ovary T	⊗	270A Liver N	422Q0606	8620	1240	57.7	65	2.2	65
42100188 (D3)	+5.9 523 Ovary T	⊗	S56 Spinal Cord N	422G0628	5894	1002	35.3	89	3.9	89
42100188 (D3)	+5.7 385A Ovary T	⊗	S91 Fetal tissue	422X0607	12151	2121	54.3	73	2.8	73
42100188 (D3)	+5.1 426A Ovary T (met)	⊗	415A Aorta N	422X0611	7487	1480	53.0	73	9.7	73
42100188 (D3)	+3.5 263A Ovary T	⊗	S73 Breast N	422H0623	7302	2116	39.2	84	4.5	84
42100188 (D3)	+3.3 383A Ovary T (met)	⊗	I1 Colon N	422B0609	3714	1113	20.4	83	2.6	83
42100188 (D3)	+3.0 933A Ovary T (SCID)	⊗	I2 Skin N	422R0601	2435	814	12.1	75	2.1	75
42100188 (D3)	+2.6 384A Ovary T (met)	⊗	272A Dendritic cell	422A0608	4578	1754	25.0	69	2.3	69
42100188 (D3)	+2.2 264A Ovary T	⊗	S2 Pancreas N	422N0629	7904	3596	38.5	81	5.6	81
42100188 (D3)	+2.0 386A Ovary T	⊗	S40 PBMC (activated)	422J0605	2191	1081	14.0	90	2.9	90
42100188 (D3)	+2.0 S115 Ovary T (met)	⊗	CT10 Small intestine	422C0604	1979	971	10.4	80	2.7	80
42100188 (D3)	+2.0 265A Ovary T	⊗	CT5 Heart N	422O0624	1911	964	13.9	93	3.4	93
42100188 (D3)	+2.0 335A Ovary T	⊗	S7 Ovary N	422O0626	1666	817	9.8	100	3.0	100
42100188 (D3)	-1.9 428A Ovary T (met)	⊗	243A Esophagus N	422A0612	1827	3480	13.4	97	9.5	97
42100188 (D3)	+1.6 261A Ovary T	⊗	S10 Skeletal muscle	42230621	5914	3653	30.4	86	6.0	86
42100188 (D3)	+1.6 266A Ovary T	⊗	S27 Ovary N	42250603	2039	1274	11.9	50	2.6	50
42100188 (D3)	+1.6 S22 Ovary T	⊗	CT19 Kidney N	42290627	1736	1072	11.0	92	4.0	92
42100188 (D3)	+1.4 9485 OT 1-P (SCID)	⊗	9485 OT 5-P (SCID)	422Y0602	4204	3074	23.0	93	7.7	93
42100188 (D3)	+1.4 262A Ovary T	⊗	334A Large Intestine	422A0622	3002	2101	16.6	89	4.0	89
42100188 (D3)	+1.3 S25 Ovary T	⊗	CT4 Bone Marrow	422H0619	1643	1297	9.6	90	3.1	90
42100188 (D3)	+1.2 429A Ovary T (met)	⊗	364A Ovary N	422I0614	2521	2084	22.0	65	23.9	65
42100188 (D3)	+1.2 382A Ovary T	⊗	CT19 Brain N	422Q0610	2072	1663	10.9	88	2.3	88
42100188 (D3)	+1.2 288A Ovary T	⊗	CT12 Lung N	422V0625	1840	1473	10.7	87	3.8	87
42100188 (D3)	+1.1 201A Ovary T	⊗	S6 Stomach N	422W0620	1329	1204	9.1	90	3.5	90

Fig. 10

Gene Name	Exp. Name	Probe 1	Probe 2	Gene ID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe1 A%	Probe2 S/B	Probe2 A%
421B0181 [C3]	+18.8 385A Ovary T	+	S91 Fetal tissue	422X0607	26711	1424	103.3	54	2.0	54
421B0181 [C3]	+11.5 S23 Ovary T	+	S56 Spinal Cord N	422G0628	13559	1179	65.3	68	3.9	68
421B0181 [C3]	+11.1 426A Ovary T (mets)	+	415A Aorta N	422X0611	14125	1273	67.3	61	5.6	61
421B0181 [C3]	+10.8 205A Ovary T	+	270A Liver N	422Q0606	16121	1488	93.1	43	2.3	43
421B0181 [C3]	+5.1 263A Ovary T	+	S73 Breast N	422H0623	11336	2235	58.2	68	4.4	68
421B0181 [C3]	+4.6 384A Ovary T (mets)	+	272A Dendritic cells	422A0608	6583	1424	24.5	40	2.1	40
421B0181 [C3]	+4.4 264A Ovary T	+	S2 Pancreas N	422N0629	9865	2245	40.9	64	3.6	64
421B0181 [C3]	+4.4 429A Ovary T (mets)	+	364A Ovary N	422I0614	2803	638	22.6	60	7.4	60
421B0181 [C3]	+4.2 261A Ovary T	+	S10 Skeletal muscle	422Z0621	8271	1949	39.5	68	3.6	68
421B0181 [C3]	+3.8 S115 Ovary T (mets)	+	C110 Small Intestine	422C0604	2281	607	11.6	60	2.1	60
421B0181 [C3]	+2.5 265A Ovary T	+	CT5 Heart N	422O0624	3192	1293	19.2	68	4.0	68
421B0181 [C3]	-2.3 S22 Ovary T	+	CT9 Kidney N	42290627	565	1276	3.6	70	3.9	70
421B0181 [C3]	+2.2 266A Ovary T	+	S27 Ovary N	42250603	2774	1260	14.3	46	2.7	46
421B0181 [C3]	+2.1 933A Ovary T (SCID)	+	I2 Skin N	422R0601	1774	837	8.4	56	2.1	56
421B0181 [C3]	+1.9 9485 OT 1-P (SCID)	+	9485 OT 5-P (SCID)	422Y0602	6967	3726	41.5	70	9.2	70
421B0181 [C3]	+1.6 382A Ovary T	+	CT19 Brain N	422Q0610	2313	1471	6.2	50	1.9	50
421B0181 [C3]	+1.6 288A Ovary T	+	CT12 Lung N	422Y0625	1657	1054	9.7	69	2.9	69
421B0181 [C3]	-1.5 S25 Ovary T	+	CT4 Bone Marrow N	422H0619	848	1243	4.5	65	2.7	65
421B0181 [C3]	+1.4 262A Ovary T	+	334A Large Intestine	422A0622	3171	2214	16.8	69	3.8	69
421B0181 [C3]	+1.2 386A Ovary T	+	S40 PBMC (activated)	422I0605	630	544	4.2	53	1.9	53
421B0181 [C3]	-1.2 335A Ovary T	+	S7 Ovary N	42220626	592	730	3.7	75	2.6	75
421B0181 [C3]	-1.0 201A Ovary T	+	S6 Stomach N	422W0620	1197	1237	7.8	65	3.5	65
421B0181 [C3]	-1.0 428A Ovary T (mets)	+	243A Esophagus N	422A0612	783	797	4.5	95	2.4	95
421B0181 [C3]	383A Ovary T (mets)	+	I1 Colon N	422B0609	3470	862	8.9	24	1.7	24

Fig. 11

Gene Name	Bal Probe 1		P1	P2 Name	Probe 2	GEM ID	Probe1		Probe2	
	Exp Name						Value	S/B	Value	S/B
42110182 (H7)	+16.7 426A Ovary T (met)	42110182 (H7)	415A Aorta N	422X0611	7706	46.3	75	462	3.5	75
42110182 (H7)	+10.7 205A Ovary T	42110182 (H7)	270A Liver N	422Q0606	10171	61.2	41	950	1.8	41
42110182 (H7)	+9.9 385A Ovary T	42110182 (H7)	S91 Fetal tissue	422X0607	14415	62.1	48	1459	2.2	48
42110182 (H7)	+8.8 S23 Ovary T	42110182 (H7)	S56 Spinal Cord N	422G0628	7781	47.3	73	880	3.4	73
42110182 (H7)	+6.4 383A Ovary T (met)	42110182 (H7)	I1 Colon N	422B0609	4807	27.6	47	748	2.2	47
42110182 (H7)	+5.1 263A Ovary T	42110182 (H7)	S73 Breast N	422H0623	9815	57.1	74	1909	4.2	74
42110182 (H7)	+4.9 429A Ovary T (met)	42110182 (H7)	364A Ovary N	422U0614	2661	20.3	61	543	6.7	61
42110182 (H7)	+3.5 264A Ovary T	42110182 (H7)	S2 Pancreas N	422N0629	7934	38.8	71	2274	3.9	71
42110182 (H7)	+2.9 S25 Ovary T	42110182 (H7)	CT4 Bone Marrow	422H0619	480	3.5	80	1375	3.0	80
42110182 (H7)	+2.8 261A Ovary T	42110182 (H7)	S10 Skeletal muscle	42230621	8993	34.6	69	3245	5.1	69
42110182 (H7)	+2.5 S115 Ovary T (met)	42110182 (H7)	CT10 Small intestine	422C0604	1864	8.1	67	738	2.2	67
42110182 (H7)	+2.3 9334 Ovary T (SCII)	42110182 (H7)	I2 Skin N	422R0601	2552	12.7	41	1113	2.6	41
42110182 (H7)	-2.3 S22 Ovary T	42110182 (H7)	CT9 Kidney N	42290627	386	3.2	69	889	3.4	69
42110182 (H7)	+2.2 384A Ovary T (met)	42110182 (H7)	272A Dendritic cell	42240608	3516	18.7	55	1567	2.2	55
42110182 (H7)	-2.2 382A Ovary T	42110182 (H7)	CT19 Brain N	422Q0610	608	4.2	60	1320	2.3	60
42110182 (H7)	+1.9 265A Ovary T	42110182 (H7)	CT5 Heart N	422Q0624	2063	13.6	87	1080	3.5	87
42110182 (H7)	+1.8 266A Ovary T	42110182 (H7)	S27 Ovary N	42250603	1550	7.0	58	847	2.1	58
42110182 (H7)	+1.5 262A Ovary T	42110182 (H7)	334A Large Intestine	422A0622	2559	13.2	73	1651	3.2	73
42110182 (H7)	-1.4 386A Ovary T	42110182 (H7)	S40 PBMC (activated)	422I0605	534	3.9	62	738	2.2	62
42110182 (H7)	-1.3 288A Ovary T	42110182 (H7)	CT12 Lung N	422V0625	893	5.3	66	1120	3.1	66
42110182 (H7)	-1.3 335A Ovary T	42110182 (H7)	S7 Ovary N	42220626	440	3.3	60	567	2.2	60
42110182 (H7)	+1.2 9485 OT 1-P (SCID)	42110182 (H7)	9485 OT 1-P (SCID)	422Y0602	4188	21.6	66	3529	9.5	66
42110182 (H7)	+1.1 428A Ovary T (met)	42110182 (H7)	243A Esophagus N	42240612	725	6.2	65	689	2.8	65
42110182 (H7)	-1.0 201A Ovary T	42110182 (H7)	S6 Stomach N	422W0620	1008	7.4	62	1018	3.2	62

Fig. 12



Gene Name	Bal Probe 1 Exp Name	P1	P2 Name	Probe 2	Gene ID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe1 A%	Probe2 S/B	Probe2 A%
421V0189 (D1)	+33.2 426A Ovary T (met)	421V0189 (D1)	415A Aorta N	422X0611	8072	243	55.2	2.4	67	2.4	67
421V0189 (D1)	+13.7 S23 Ovary T	421V0189 (D1)	S56 Spinal Cord N	422X0628	7367	537	42.6	2.5	69	2.5	69
421V0189 (D1)	+12.6 429A Ovary T (met)	421V0189 (D1)	364A Ovary N	422X0614	2850	227	21.7	3.5	64	3.5	64
421V0189 (D1)	+8.0 385A Ovary T	421V0189 (D1)	S91 Fetal tissue	422X0607	11711	1469	54.0	2.2	58	2.2	58
421V0189 (D1)	+7.3 263A Ovary T	421V0189 (D1)	S73 Breast N	422H0623	6949	952	37.8	2.6	69	2.6	69
421V0189 (D1)	-5.8 S25 Ovary T	421V0189 (D1)	CT14 Bone Marrow	422H0619	208	1210	2.1	2.9	44	2.9	44
421V0189 (D1)	+5.0 205A Ovary T	421V0189 (D1)	270A Liver N	422X0606	8676	1737	52.3	2.6	57	2.6	57
421V0189 (D1)	+4.5 383A Ovary T (met)	421V0189 (D1)	I1 Colon N	422B0609	3149	707	17.4	2.0	57	2.0	57
421V0189 (D1)	+4.4 261A Ovary T	421V0189 (D1)	S10 Skeletal muscle	422X0621	6332	1443	29.1	2.9	77	2.9	77
421V0189 (D1)	+4.2 264A Ovary T	421V0189 (D1)	S2 Pancreas N	422N0629	7612	1809	38.1	3.3	79	3.3	79
421V0189 (D1)	-3.2 382A Ovary T	421V0189 (D1)	CT19 Brain N	422Q0610	468	1508	3.4	2.3	60	2.3	60
421V0189 (D1)	+2.9 933A Ovary T (SCID)	421V0189 (D1)	I2 Skin N	422R0601	2500	860	12.3	2.1	51	2.1	51
421V0189 (D1)	+2.5 S115 Ovary T (met)	421V0189 (D1)	CT10 Small intestine	422C0604	1424	569	6.7	2.1	61	2.1	61
421V0189 (D1)	+2.4 265A Ovary T	421V0189 (D1)	CT5 Heart N	422C0624	1742	723	11.8	2.8	70	2.8	70
421V0189 (D1)	+2.3 384A Ovary T (met)	421V0189 (D1)	272A Dendritic cell	42240608	3083	1342	17.0	2.0	62	2.0	62
421V0189 (D1)	+1.9 266A Ovary T	421V0189 (D1)	S27 Ovary N	422S0603	1370	732	8.0	2.0	47	2.0	47
421V0189 (D1)	-1.9 386A Ovary T	421V0189 (D1)	S40 PBMC (active)	422A0605	307	580	2.6	2.0	41	2.0	41
421V0189 (D1)	+1.7 262A Ovary T	421V0189 (D1)	334A Large Intestine	422A0622	2097	1202	11.2	2.7	86	2.7	86
421V0189 (D1)	-1.3 335A Ovary T	421V0189 (D1)	S7 Ovary N	422D0626	373	470	2.9	2.0	47	2.0	47
421V0189 (D1)	-1.1 288A Ovary T	421V0189 (D1)	CT12 Lung N	422Y0625	969	1094	5.6	2.9	72	2.9	72
421V0189 (D1)	+1.1 201A Ovary T	421V0189 (D1)	S6 Stomach N	422W0620	750	672	5.6	2.4	62	2.4	62
421V0189 (D1)	+1.1 428A Ovary T (met)	421V0189 (D1)	243A Esophagus N	42240612	498	446	4.2	2.1	73	2.1	73
421V0189 (D1)	-1.0 9485 OT 1-P (SCID)	421V0189 (D1)	9485 OT 5-P (SCID)	422Y0602	3117	3174	16.7	8.2	91	8.2	91
421V0189 (D1)	522 Ovary T	421V0189 (D1)	CT19 Kidney N	42290627	224	409	2.3	2.3	48	2.3	48

Fig. 13

Gene Name	Exp Name	Probe 1	P1	P2 Name	Probe 2	GEN ID	Probe1 Value	Probe2 Value	Probe1 S/B	Probe1 A%	Probe2 S/B	Probe2 A%
421H0187 [E11]	+20.2 426A Ovary T (met)	421H0187 [E11]	421H0187 [E11]	415A Aorta N	422X0611	422X0611	5441	270	36.3	50	2.3	50
421H0187 [E11]	+10.0 523 Ovary T	421H0187 [E11]	421H0187 [E11]	S36 Spinal Cord N	422C0628	422C0628	5318	533	27.1	56	2.3	56
421H0187 [E11]	+8.3 429A Ovary T (met)	421H0187 [E11]	421H0187 [E11]	364A Ovary N	422U0614	422U0614	1252	130	10.1	58	2.5	58
421H0187 [E11]	+5.7 385A Ovary T	421H0187 [E11]	421H0187 [E11]	S91 Fetal tissue	422X0607	422X0607	9507	1668	35.8	45	2.1	45
421H0187 [E11]	+4.4 205A Ovary T	421H0187 [E11]	421H0187 [E11]	270A Liver N	422Q0606	422Q0606	5456	1235	31.1	50	2.0	50
421H0187 [E11]	+4.2 265A Ovary T	421H0187 [E11]	421H0187 [E11]	CT5 Heart N	422Q0624	422Q0624	1834	438	11.9	48	2.0	48
421H0187 [E11]	-4.1 382A Ovary T	421H0187 [E11]	421H0187 [E11]	CT19 Brain N	422Q0610	422Q0610	309	1259	2.6	48	2.0	48
421H0187 [E11]	+3.6 261A Ovary T	421H0187 [E11]	421H0187 [E11]	S10 Skeletal muscle	42230621	42230621	3733	1036	17.7	55	2.3	55
421H0187 [E11]	+3.4 263A Ovary T	421H0187 [E11]	421H0187 [E11]	S73 Breast N	422H0623	422H0623	4163	1239	23.0	62	3.0	62
421H0187 [E11]	+2.5 5115 Ovary T (met)	421H0187 [E11]	421H0187 [E11]	CT10 Small intestine	422C0604	422C0604	1565	627	8.8	47	2.1	47
421H0187 [E11]	+2.1 264A Ovary T	421H0187 [E11]	421H0187 [E11]	S2 Pancreas N	422N0629	422N0629	3455	1630	14.9	60	3.0	60
421H0187 [E11]	+2.1 384A Ovary T (met)	421H0187 [E11]	421H0187 [E11]	272A Dendritic cell	42240608	42240608	2667	1270	13.4	44	1.9	44
421H0187 [E11]	-2.1 522 Ovary T	421H0187 [E11]	421H0187 [E11]	CT9 Kidney N	42290627	42290627	291	605	2.4	51	2.5	51
421H0187 [E11]	-1.7 386A Ovary T	421H0187 [E11]	421H0187 [E11]	S40 PBMC (activated)	422J0605	422J0605	410	687	3.2	47	2.0	47
421H0187 [E11]	+1.6 9334 Ovary T (SCII)	421H0187 [E11]	421H0187 [E11]	I2 Skin N	422R0601	422R0601	1622	984	7.9	44	2.2	44
421H0187 [E11]	+1.5 262A Ovary T	421H0187 [E11]	421H0187 [E11]	334A Large Intestine	422A0622	422A0622	1892	1245	10.1	50	2.6	50
421H0187 [E11]	-1.5 288A Ovary T	421H0187 [E11]	421H0187 [E11]	CT12 Lung N	422V0625	422V0625	604	908	4.1	62	2.6	62
421H0187 [E11]	-1.4 428A Ovary T (met)	421H0187 [E11]	421H0187 [E11]	243A Esophagus N	42240612	42240612	236	325	2.7	78	1.9	78
421H0187 [E11]	-1.3 335A Ovary T	421H0187 [E11]	421H0187 [E11]	S7 Ovary N	42220626	42220626	382	501	2.9	58	2.0	58
421H0187 [E11]	-1.2 201A Ovary T	421H0187 [E11]	421H0187 [E11]	S6 Stomach N	422W0620	422W0620	558	677	4.2	58	2.3	58
421H0187 [E11]	+1.0 9485 OT 1-P (SCID)	421H0187 [E11]	421H0187 [E11]	9485 OT 5-P (SCID)	422Y0602	422Y0602	2582	2493	15.1	57	6.3	57
421H0187 [E11]	383A Ovary T (met)	421H0187 [E11]	421H0187 [E11]	I1 Colon N	422B0609	422B0609	2261	562	12.5	38	1.7	38
421H0187 [E11]	266A Ovary T	421H0187 [E11]	421H0187 [E11]	S27 Ovary N	42250603	42250603	1739	965	9.7	36	2.2	36
421H0187 [E11]	S25 Ovary T	421H0187 [E11]	421H0187 [E11]	CT4 Bone Marrow	422H0619	422H0619	283	845	2.2	44	2.2	44

Fig. 14

11721-1

ACGGTTTCAATGGACACTTTTTATTGTTTACTTAATGGATCATCAATTTTGTCTCACTACCTACAAATGGAATTT  
CATCTTGTTTCCATGCTGAGTAGTGAAACAGTGACAAAGCTAATCATAATAACCTACATCAAAAGAGAACTAA  
GCTAACACTGCTCACTTTCTTTTTAACAGGCAAAATATAAATATATGCACTCTAXAATGCACAATGGTTTAGT  
CACTAAAAAATTCAAATGGGATCTTGAAGAATGTATGCAAATCCAGGGTGCAGTGAAGATGAGCTGAGATG  
CTGTGCAACTGTTTAAAGGGTTCCTGGCACTGCATCTCTTGCCACTAGCTGAATCTTGACATGGAAGGTTTT  
AGCTAATGCCAAGTGGAGATGCAGAAAATGCTAAGTTGACTTAGGGGCTGTGCACAGGAACTAAAAGGCGAG  
GAAAGTACTAAATATTGCTGAGAGCATCCACCCAGGAAGGACTTTACCTTCCAGGAGCTCCAAACTGGCA  
CCACCCCCAGTGCTCACATGGCTGACTTTATCCTCCGTGTTCCATTTGGCACAGCAAGTGGCAGT

11721-2

AAGGCTGGTGGGTTTTTGATCCTGCTGGAGAACCTCCGCTTTCATGTGGAGGAAGAAGGGAAGGGAAAAG  
ATGCTTCTGGGAACAAGGTTAAAGCCGAGCCAGCCAAAATAGAAGCTTTCGAGCTTCACCTTCCAAGCTA  
GGGGATGTCTATGTCAATGATGCTTTTGGCACTGCTCACAGAGCCACAGCTCCATGGTAGGAGTCAATCT  
GCCACAGAAGGCTGGTGGGTTTTTGATGAAGAAGGAGCTGAACCTACTTTGCAAAGGCCTTGGAGAGCCCA  
GAGCGACCCTTCCTGGCCATCCTGGGCGGAGCTAAAGTTGCAGACAAGATCCAGCTCATCAATAATATGCT  
GGACAAAGTCAATGAGATGATTATTGGTGGTGGAAATGGCTTTACCTTCCTTAAGGTGCTCAACAACATGGA  
GATTGGCACTTCTCTGTTTGATGAAGAGGGAGCCAAGATTGTCAAAGACCTAATGTCCAAAGCTGAGAAGA  
ATGGTGTGAAGATTACCTTGCCTGTTGACTTTGTCACTGCTGACAAGTTTGATGA

11724-1

TTTGTTCCCTTACATTTTTCTAAAGAGTTACTTAAATCAGTCAACTGGTCTTTGAGACTCTTAAGTTCTGATTCC  
AACTTAGCTAATTCATTCTGAGAACTGTGGTATAGGTGGCGTGTCTCTTCTAGCTGGGACAAAAGTTCTTTG  
TTTTCCCCCTGTAGAGTATCACAGACCTTCTGCTGAAGCTGGACCTCTGTCTGGGCCTTGGACTCCCAAT  
CTGCTTGTCTGTTCAAGCCTGGAAATGTTAATCTTTAATCTTCCATATGGATGGACATCTGTCTAAGTTGA  
TCCTTTAGAACACTGCAATTATCTTCTTTGAGTCTAATTTCTTCTTTGCTTTGAATCGCATCACTAACTT  
CCTCTCCCATTCTTAGCTTCATCTATCACCCCTGTCACGATCATCCTGGAGGGAAGACATGCTCTTAGTAAA  
GGCTGCAAGCTGGGTACAGTACTGTCCAAGTTTTCTGAAGTTGCTGAACTTCCTTGTCTTTCTTGTTCAA  
AGTAACCTGAATCTCTCCAATTGTCTCTTCCAAGTGGACTTTTTCTCTGCGCAAAGCATCCAG

11724-2

TCATTGCCTGTGATGGCATCTGGAATGTGATGAGCAGCCAGGAAGTTGTAGATTTCAATCAATCAAAGGATT  
CAGCATGTGGTGGAAGCTGTGAGGCAAGAGAAACAAGAACTGTATGGCAAGTTAAGAAGCACAGAGGCAA  
ACAAGAAGGAGACAGAAAAGCAGTTGCAGGAAGCTGAGCAAGAAATGGAGGAAATGAAAGAAAAGATGAG  
AAAGTTTGCTAAATCTAAACAGCAGAAAATCCTAGAGCTGGAAGAAGAGAATGACCGGCTTAGGGCAGAGG  
TGCACCCTGCAGGAGATACAGCTAAAGAGTGTATGGAAACACTTCTTTCTTCCAATGCCAGCATGAAGGAA  
GAACTTGAAAGGGTCAAAATGGAGTATGAAACCCTTTCTAAGAAGTTTCAGTCTTTAATGTCTGAGAAAGAC  
TCTCTAAGTGAAGAGGTTCAAGATTTAAAGCATCAGATAGAAGGTAATGTATCTAAACAAGCTAACCTAGAG  
GCCACCGAGAAACATGATAACCAACGAATGTCACTGAAGAGGGAACACAGTCTATACCAGGT

**11725-32-1.2**

AAGCCAATAATCACCATTTATTACTTAATATATGCCAACCACTGTACTTGGCAGTTCACAAATTCTCACCGTT  
ACAACAACCCCATGAGGTATTTATTCCCATTTCTATAGATAGGGAAACCACAGCTCAAGTAAGTTAGGAACT  
GAGCCAAGTATACACAGAATACGAAGTGGCAAACCTAGAAGGAAAGACTGACACTGCTATCTGCTGGCCTC  
CAGTGTCCCTGGCTCTTTTCACACGGGTCATGTCTCCAGCGCTGCTGCTGCTGCTGCATTACCATGCCCTC  
ATTGTTTTCTTCCCTCTGGTGTCAACTGCATCCTTCAAAGAATCTAACTCATTCCAGAGACCACTTATTTCTT  
TCTCTCTTTCTGAAATTACTTTTAATAATTCTTCATGAGGGGGAAAAGAAGATGCCTGTTGGTAGTTTTGTTG  
TTTAAGCTGCTCAATTTGGGACTTAAACAATTTGTTTTCATCTTGTACATCCTGTAACAGCTGTGTTTTGCTA  
GAAAGATCACTCTCCCTCTCTTTTAGCATGGCTTCTAACCTCTTCAATTCATTTTCCTTTCTTTCAACACAAT  
CTCAAGTTCTTCAAACCTGTGATGCAGAAGAGGCCTCTTTCAAGTTATGTTGTGCTACTTCCTGAACATGTGC  
TTTTAAAGATTCATTTTCTTCTTGAAGATCCTGTAACCACTTCCCTGTATTGGCTAGGTCTTTCTTTCTCTT  
CCAAAACAGCCTTCATGGTATTCATCTGTTCTCTTTCTTTTAATAAGTTCAGGAGCTTCAGAAC

**11726-1&2**

CAAGCTTTTTTTTTTTTTTTTTAAAAAGTGTTAGCATTAAATGTTTTATTGTACGCAGATGGCAACTGGGTTTTATG  
TCTTCATATTTTATATTTTTGTAAATTAATAAATTACAAGTTTTAAATAGCCAATGGCTGGTTATATTTTCAGA  
AAACATGATTAGACTAATTCATTAATGGTGGCTTCAAGCTTTTCCTTATTGGCTCCAGAAAATTCACCCACCT  
TTTGTCCCTTCTTAAAAAAGTGAATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTC  
ATCCACATCTACTTCAAGGAATATCACGTTGGAATACTTTTCAGAGAGGGAATGAAAGAAAGGCTTGATCAT  
TTTGCAAGGCCACACCACGTGGCTGAGAAGTCAACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTT  
CCTGAAAAGCAGTCTTGCTCTCGATCTGCTTACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGG  
ACCGATGGAAATGGATCCAAAGCACCAAACAGAGCTTCAAGACTCGCTGCTTGGCTTGAATTCGGATCCGA  
TATCGCCATGGCCT

**11727-1&2**

AAGTGTTAGCATTAAATGTTTTATTGTACGCAGATGGCAACTGGGTTTTATGTCTTCATATTTTATATTTTGT  
AATTAATAAATTMCAAGTTTTAAATAGCCAATGGCTGGTTATATTTTCAGAAAACATGATTAGACTAATTCAT  
TAATGGTGGCTTCAAGCTTTTCCTTATTGGCTCCAGAAAATTCACCCACCTTTTGTCCCTTCTTAAAAAAGT  
GAATGTTGGCATGCATTTGACTTCACACTCTGAAGCAACATCCTGACAGTCATCCACATCTACTTCAAGGAA  
TATCACGTTGGAATACTTTTCAGAGAGGGAATGAAAGAAAGGCTTGATCATTTTGCAAGGCCACACCACGT  
GGCTGAGAAGTCAACTACTACAAGTTTATCACCTGCAGCGTCCAAGGCTTCTGAAAAGCAGTCTTGCTCT  
CGATCTGCTTACCATCTTGGCTGCTGGAGTCTGACGAGCGGCTGTAAGGACCGATGGAAATGGATCCAA  
GCACCAAACAGAGCTTCAAGACTCGCTGCTTGGCATGAATTCGGATCCGA

11728.1.40.19.19

TACAAACTTTATTGAAACGCACACGCGCACACACACAAACACCCCTGTGGATAGGGAAAAGCACCTGGCCA  
CAGGGTCCACTGAAACGGGGAGGGGATGGCAGCTTGTAATGTGGCTTTGCCACAACCCCTTCTGACAG  
GGAAGGCCTTAGATTGAGGCCCCACCTCCCATGGTGATGGGGAGCTCAGAATGGGGTCCAGGGAGAATTT  
GGTTAGGGGGAGGTGCTAGGGAGGCATGAGCAGAGGGCACCCCTCCGAGTGGGGTCCCGAGGGCTGCAG  
AGTCTTCAGTACTGTCCCTCACAGCAGCTGTCTCAAGGCTGGGTCCCTCAAAGGGGGCGTCCCAGCGCGGG  
GCCTCCCTGCGCAAACACTTGGTACCCCTGGCTGCGCAGCGGAAGCCAGCAGGACAGCAGTGGCGCCGA  
TCAGCACAACAGACGCCCTGGCGGTAGGGACAGCAGGCCAGCCCTGTCGGTTGTCTCGGCAGCAGGTC  
TGGTTATCATGGCAGAAGTGTCTTCCCACACTTCACGTCCTTACACCCACGTGAXGGCTACXGGCCAGG  
AAG

11728.2.40.19.19

CCCGTGGGTGCCATCCACGGAGTTGTTACCTGATCTTTGGAAGCAGGATCGCCCGTCTGCACTGCAGTGG  
AAGCCCCGTGGGCAGCAGTGATGGCCATCCCCGCATGCCACGGCCTCTGGGAAGGGGCAGCAACTGGAA  
GTCCCTGAGACGGTAAAGATGCAGGAGTGGCCGGCAGAGCAGTGGGCATCAACCTGGCAGGGGGCCACCC  
AGATGCCTGCTCAGTGTTGTGGGCCATTTGTCCAGAAAGGGGACGGCAGCAGCTGTAGCTGGCTCCTCCGG  
GGTCCAGGCAGCAGGCCACAGGGCAGAACTGACCATCTGGGCACCGCGTTCCAGCCACCAGCCCTGCTG  
TTAAGGCCACCCAGCTCACCAGGGTCCACATGGTCTGCCTGCGTCCGACTCCGCGGTCTTGGGCCCTGA  
TGGTTCTACCTGCTGTGAGCTGCCCAGTGGGAAGTATGGCTGCTGCCAATGCCCAACGCCACCTGCTGCT  
CCGATCACCTGCACTGCTGCCCCAAGACACTGTGTGTGACCTGATCCAGAGTAAGTGCCTCTCCAAGGAGA  
ACG

11730-1

GAATCACCTTTCTGGTTTAGCTAGTACTTTGTACAGAACAAATGAGGTTTCCCACAGCGGAGTCTCCCTGGGC  
TCTGTTTGGCTCTCGGTAAGGCAGGCCTACACCTTTTCTCTCTCTATGGAGAGGGGAATATGCATTAAG  
GTGAAAAGTCACCTTCCAAAAGTGAGAAAGGGATTGATTGCTGCTTCAGGACTGTGGAATTATTTGGAATG  
TTTTACAAATGTTGCTACAAAACAACAAAAAAGGTAATTACAAATGTGTACATCACAACATGCTTTTTAA  
GACATTATGCATTGTGCTCACATTCCCTTAAATGTTGTTTCCAAAGGTGCTCAGCCTCTAGCCCAGCTGGAT  
TCTCCGGGAAGAGGCAGAGACAGTTTGGCGAAAAAGACACAGGGAAGGAGGGGGTGGTGAAGGAGAAA  
GCAGCCTTCCAGTTAAAGATCAGCCCTCAGTTAAAGGTCAGCTTCCCGCAXGCTGGCCTCAXGCGGAGTCT  
GGGTCAGAGGGAGGAGCAGCAGCAGGGTGGGACTGGGGCGT

11730-2

AACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGC  
AAGATCCAGGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTT  
GAGGGAGAAAGGCGGGGGCCGGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTG  
GTTGAAGAAGAGCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAA  
AAGCTGCTGATGAGAGTGAGAGAGGTATGAAGGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATG  
GAACTCCAGGAAATCCAACCTCAAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGT  
GGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGAGTCC  
CGTTGCCGAGAGATGGATGAGCAGATTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

**11732.1contig**

GAGAACTTGGCCTTTATTGTGGGCCCAGGAGGGCACAAAGGTCAGGAGGCCCAAGGGAGGGATCTGGTTT  
TCTGGATAGCCAGGTCATAGCATGGGTATCAGTAGGAATCCGCTGTAGCTGCACAGGCCTCACTTGCTGCA  
GTTCCGGGGAGAACACCTGCACTGCATGGCGTTGATGACCTCGTGGTACACGACAGAGCCATTGGTGCA  
TGCAAGGGGCACGCGCATGGGCTCCGTCCTCGAGGGCAGGCAGCAGGAGCATTGCTCCTGCACATCCTCG  
ATGTCAATGGAGTACACAGCTTTGCTGGCACACTTTCCCTGGCAGTAATGAATGTCCACTTCCTCTTGGGAC  
TTACAATCTCCCACTTTGATGTACTGCACCTTGGCTGTGATGTCTTTGCAATCAGGCTCCTCACATGTGTCA  
CAGCAGGTGCCTGGAATTTTCACGATTTTGCCTCCTTCAGCCAGACACTTGTGTTTCATCAAATGGTGGGCA  
GCCCGTGACCCTCTTCTCCAGATGTACTCTCCTCT

**11732.2contig**

GCCTGGACCTTGCCGGATCAGTGCCACACAGTGACTTGCTTGGCAAATGGCCAGACCTTGCTGCAGAGTC  
ATCGTGTCAATTGTGACCATGGACCCCGGCTTCATGTGCCAACAGCCAGTCTCCTGTTCCGGGTGGAGGA  
GACGTGTGGCTGCCGCTGGACCTGCCCTTGTGTGTGCACGGGCAGTTCCACTCGGCACATCGTCACCTTC  
GATGGGCAGAATTTCAAGCTTACTGGTAGCTGCTCCTATGTATCTTTCAAACAAGGAGCAGGACCTGGA  
AGTGCTCCTCCACAATGGGGCCTGCAGCCCCGGGGCAAACAAGCCTGCATGAAGTCCATTGAGATTAAG  
CATGCTGGCGTCTCTGCTGAGCTGCACAGTAACATGGAGATGGCAGTGGATGGGAGACTGGTCTTGCCC  
CGTACGTTGGTGAAAACATGGAAGTCAGCATCTACGGCGCTATCATGTATGAAGTCAGGTTTACCCATCTTG  
GCCACATCCTCACATACACCGCCXCAAACAACGAGTT

**11735-1-2**

AGATCAACCTCTGCTGGTCAGGAGGAATGCCTTCCTTGTCTTGGATCTTTGCTTTGACGTTTCTCGATAGTRW  
CAaCTKKRYTSRAMSKMAAGKGYRATGRWMTTKSYWGWRSYKTMWWWMRSGRARAYTTaGaCAYCCCMC  
CTCWgAGaCGSAGKACCARGTGCAgAgGTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTGCGTCCATC  
TTCCAGCTGTTTCCAGCAAAGATCAACCTCTGCTGATCAGGAGGGATGCCTTCCTTATCTTGGATCTTTGC  
CTTGACATTCTCGATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTCTTCACGA  
AGATYTGATCCACCTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTAGTCAGAC  
AGGGTGCGYCCATCTTCCAGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATGCCTTCCT  
TGTCYTGATCTTTGCTTGGACRTTCTCRATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTCTTACCAG  
TCAGGGTCTTCACGAAGATCTGCATCCACCTCTAA

**11740.2.contig**

AAGTCACAAACAGACAAAGATTATTACCAGCTGCAAGCTATATTAGAAGCTGAACGAAGAGACAGAGGTCAT  
GATTCTGAGATGATTGGAGACCTTCAAGCTCGAATTACATCTTTACAAGAGGAGGTGAAGCATCTCAAACAT  
AATCTCGAAAAAGTGGAAGGAGAAAGAAAAGAGGCTCAAGACATGCTTAATCACTCAGAAAAGGAAAAGAA  
TAATTTAGAGATAGATTTAACTACAACTTAAATCATTACAACAACGGTTAGAACAAGAGGTAAATGAACAC  
AAAGTAACCAAAGCTCGTTTAACTGACAAACATCAATCTATTGAAGAGGCAAAGTCTGTGGCAATGTGTGAG  
ATGGAAAAAAGCTGAAAGAAGAAAGAGAAGCTCGAGAGAAGGCTGAAAATCGGGTTGTTTCAGATTGAGAA  
ACAGTGTTCCATGCTAGACGTTGATCTGAAGCAATCTCAGCAGAACTAGAACATTTGACTGGAATAAAGA  
AAGGATGGAGGATGAAGTTAAGAATCTA

**11765.2&64.2.contig**

CGCCTCCACCATGTCCATCAGGGTGACCCAGAAGTCCTACAAGGTGTCCACCTCTGGCCCCGGGCCTTC  
AGCAGCCGCTCCTACACGAGTGGGCCCCGGTTCCCGCATCAGCTCCTCGAGCTTCTCCCGAGTGGGCAGCA  
GCAACTTTTCGCGGTGGCCTGGGCGGCGGCTATGGTGGGGCCAGCGGCATGGGAGGCATCACCGCAGTTA  
CGGTCAACCAGAGCCTGCTGAGCCCCCTTGCTCTGGAGGTGGACCCCAACATCCAGGCCGTGCGCACCC  
AGGAGAAGGAGCAGATCAAGACCCTCAACAACAAGTTTGCCTCCTTCATAGACAAGGTACGGTTCCTGGAG  
CAGCAGAACAAGATGCTGGAGACCAAGTGGAGCCTCCTGCAGCAGCAGAAGACGGCTCGAAGCAACATGG  
ACAACATGTTTCGAGAGCTACATCAACARCTTAGGCGGCAGCTGGAGACTCTGGGCCAGGAGAAGCTGAA  
GCTGGAGGCGGAGCTTGGCAACATGCAGGGGGCTGGTGGAGGACTTCAAGAACAAGTATGAGGATGAGATC  
AATAAGCGTACAGAGATGGAGAACGAATTTGCTCTCATCAAGAAGGATGTGGATGAAGCTTACATGAACAA  
GGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGACGAGATCAACTTCCTCAGGCAGCTGTATGAAGAG  
GAGATCCGGGAGCTGCAGTCCCAGATCTCGGACACATCTGTGGTGTGTCCATGGACAACAGCCGCTCCC  
TGGACATGGACAGCATCATTGCTGAGGTCAAGGCACAGTACGAGGATATTGCCAACCGCAGCCGGGCTGA  
GGCTGAGAGCATGTACCAGGTCAAGTATGAGGAGCTGCAGAGCCTGGCTGGGAAGCACGGGGATGACCT  
GCGGCGCACAAAGACTGAGATCTCTGAGATGAACCGGAACATCAGCCCCGGCTXCAGGCTGAGATTGAGG  
GCCTCAAAGGCCAGAXGGCTTXCCTGGAXGXCCGCCAT

**11767.2.contig**

CCCGGAGCCAGCCAACGAGCGGAAAATGGCAGACAATTTTCGCTCCATGATGCGTTATCTGGGTCTGGAA  
ACCCAAACCCTCAAGGATGGCCTGGCGCATGGGGGAACCAGCCTGCTGGGGCAGGGGGCTACCCAGGG  
GCTTCCTATCCTGGGGCCTACCCCGGGCAGGCACCCCGAGGGGCTTATCCTGGACAGGCACCTCCAGGC  
GCCTACCCTGGAGCACCTGGAGCTTATCCCGGAGCACCTGCACCTGGAGTCTACCCAGGGGCCACCCAGC  
GGCCCTGGGGCCTACCCATCTTCTGGACAGCCAAGTGCCACCGGAGCCTACCCTGCCACTGGCCCCCTATG  
GCGCCCCTGCTGGGCCACTGATTGTGCCTTATAACCTGCCTTTGCCTGGGGGAGTGGTGCCTCGCATGCT  
GATAACAATTCTGGGCACGGTGAAGCCCAATGCAAACAGAATTGCTTTAGATTTCCAAAGAGGGAATGATGT  
TGCCTTCCACTTTAACCACGCTTCAATGAGAACAACAGGAGAGTCATTGGTTGCAATACAAAGCTGGATAA

**11768-1&2**

GGGAATGCAACAACCTTTATTGAAAGGAAAGTGCAATGAAATTTGTTGAAACCTTAAAAGGGGAACTTAGAC  
ACCCCCCTCRAgCGMAGKACCARGTGCAAgGTGGACTCTTTCTGGATGTTGTAGTCAGACAGGGTRCG  
WCCATCTTCCAGCTGTTTYCCRGCAAAGATCAACCTCTGCTGATCAGGAGGRATGCCTTCCTTATCTTGGA  
TCTTTGCCTTGACATTCTCGATGGTGTCACTGGGCTCCACCTCGAGGGTGATGGTCTTACCAGTCAGGGTC  
TTCACGAAGATYTGATCCACCTCTGAGACGGAGCACCAGGTGCAGGGTRGACTCTTTCTGGATGTTGTA  
GTCAGACAGGGTGCGYCCATCTTCCAGCTGcTTTCCSaGCAAAGATCAACCTCTGCTGGTCAGGAGGRATG  
CCTTCCTTGTCTYGGATCTTTCYTTGACRTTCTCAATGGTGTCACTCGGCTCCACTTCGAGAGTGATGGTC  
TTACCAGTCAGGGTCTTACGAAGATCTGCATCCACCTCTAAGACGGAGCACCAGGTGCAGGGTGGACT  
CTTTCTGGATGgTTGTAGTCAGACAGGGTGCGTCCATCTTCCAGCTGTTTCCCAGCAAAGATCAACCT

**11768-1&2-11735-1&2**

AGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAAcCATCCAGAAAGAGT  
CCACCCTGCACCTGGTGTCTCCGTCTTAGAGGTGGGATGCAGATCTTCGTGAAGACCCTGACTGGTAAGAC  
CATCACTCTCGAAGTGGAGCCGAGTGACACCATTGAGAAyGTCAARGCAAAGATCCARGACAAGGAAGGC  
ATYCCTCCTGACCAGCAGAGGTTGATCTTTGcISGGAAAgCAGCTGGAAGATGGRCGCACCCTGTCTGACTA  
CAACATCCAGAAAGAGTCYACCCTGCACCTGGTGTCTCCGTCTCAGAGGTGGGATGCGARATCTTCGTGAAGA  
CCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCCAGTGACACCATCGAGAATGTCAAGGCCAAAGAT  
CCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTTTGCTGGGAAACAGCTGGAAGATGGAC  
GCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACcTYTGACyTGGTMCTBCGtCTYaGAGGKGGGRTG  
caaaTCTWMGtKWagaCaCtCaCTKKYAAGRYyATCAMCMWtGAKKTCgAKYSCASTKWCaCTWTCRAKAAMGT  
YRWWGCAWagaTCCMAGACAAGGAAGGCATTCTCTGACCAGCAGAGGTTGATCT

**11769.1.contig**

ATGGAGTCTCACTCTGTGCGACCAGGCTGGAGCGCTGTGGTGCGATATCGGCTCACTGCAGTCTCCACTTC  
CTGGGTTCAAGCGATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCAGGCGTCACCATAATTT  
TTGTATTTTTAGTAGAGACATGGTTTCGCCATGTTGGCTGGGCTGGTCTCGAACTCCTGACCTCAAGTGATC  
TGTCCTGGCCTCCCAAAGTGTTGGGATTACAGGCGAAAGCCAACGCTCCCGGCCAGGGAACAACCTTTAGA  
ATGAAGGAAATATGCAAAAGAACATCACATCAAGGATCAATTAATTACCATCTATTAATTACTATATGTGGGT  
AATTATGACTATTTCCCAAGCATTCTACGTTGACTGCTTGAGAAGATGTTTGTCTGCATGGTGGAGAGTG  
AGAAGGGCCAGGATTCTTAGGTT

**11769.2.contig**

AGCGCGGTCTTCCGGCGCGAGAAAGCTGAAGGTGATGTGGCCGCCCTCAACCGACGCATCCAGCTCGTT  
GAGGAGGAGTTGGACAGGGCTCAGGAACGACTGGCCACGGCCCTGCAGAAGCTGGAGGAGGCAGAAAAA  
GCTGCAGATGAGAGTGAGAGAGGAATGAAGGTGATAGAAAACCGGGCCATGAAGGATGAGGAGAAGATGG  
AGATTCAGGAGATGCAGCTCAAAGAGGCCAAGCACATTGCGGAAGAGGCTGACCGCAAATACGAGGAGGT  
AGCTCGTAAGCTGGTCATCCTGGAGGGTGAGCTGGAGAGGGCAGAGGAGCGTGCGGAGGTGTCTGAACT  
AAAATGTGGTGACCTGGAAGAAGAACTCAAGAATGTTACTAACAATCTGAAATCTCTGGAGGCTGCATCTGA  
AAAGTATTCTGAAAAGGAGGACAAATATGAAGAAGAAATTAACCTTCTGTCTGACAACTGAAAGAGGCTGA  
GACCCGTGCTGAATTTGCAGAGAGAACGGTTGCAAACCTGGAAGAGACAATTGATGACCTGGAAGAGAAAC  
TTGCCACGC

**11770.1.contig**

GTGCACAGGTCCCATTTATTGTAGAAAATAATAAATTACAGTGATGAATAGCTCTTCTTAAATTACAAAAC  
AGAAACCACAAAGAAGGAAGAGGAAAAACCCAGGACTTCCAAGGGTGAAGCTGTCCCCTCCTCCCTGCC  
ACCCTCCCAGGCTCATTAGTGTCCTTGGAAGGGGCAGAGGACTCAGAGGGGATCAGTCTCCAGGGGGCCCT  
GGGCTGAAGCGGGTGAGGCAGAGAGTCCTGAGGCCACAGAGCTGGGCAACCTGAGCCGCCTCTCTGGCC  
CCCTCCCCCACCCTGCCCCAACCTGTTTACAGCACCTTCGCCCCCTCCCCTCTAAACCCGTCCATCCACTC  
TGCACTTCCCAGGCAGGTGGGTGGGCCAGGCCTCAGCCATACTCCTGGGCGCGGGTTTCGGTGAGCAAG  
GCACAGTCCCAGAGGTGATATCAAGGCCT



**11770.2.contig**

GCAAGGAAGTGGTCTGCTCACACTTGCTGGCTTGCGCATCAGGACTGGCTTTATCTCCTGACTCACGGTGCA  
AAAGGTGCACTCTGCGAACGTTAAGTCCGTCCCCAGCGCTTGGAATCCTACGGCCCCACAGCCGGATCC  
CCTCAGCCTTCCAGGTCTCAACTCCCGTGGACGCTGAACAATGGCCTCCATGGGGCTACAGGTAATGGG  
CATCGCGCTGGCCGCTCTGGGCTGGCTGGCCGTCATGCTGTGCTGCGCGCTGCCCATGTGGCGCGTGAC  
GGCCTTCATCGGCAGCAACATTGTACCTCGCAGACCATCTGGGAGGGCCTATGGATGAACTGCGTGGTG  
CAGAGCACCGGCCAGATGCAGTGCAAGGTGTACGACTCGCTGCTGGCACTGCCGAGGACCTGCAGGCG  
GCCCCGCGCCCTCGTCATCATCA

**11773.1.contig**

TGCAAAAGGGACACAGGGGTTCAAAAATAAAAATTTCTCTTCCCCCTCCCCAAACCTGTACCCCAGCTCCC  
CGACCACAACCCCTTCTCTCCCCGGGGAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGAAGA  
GAGAGGCCGGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTCCAAATATAAATACXTGTGTGAGAACTGGA  
AAATCCTCCAGCACCCACCACCAAGCACTCTCCGTTTTCTGCCGGTGTGGGAGAGGGGCGGGGGGCAG  
GGGCGCCAGGCACCGGCTGGCTGCGGTCTACTGCATCCGCTGGGTGTGCACCCCGCGAGCCTCCTGCTG  
CTCATTGTAGAAGAGATGACACTCGGGGTCCCCCGGATGGTGGGGGCTCCCTGGATCAGCTTCCCGGTG  
TTGGGGTTACACACCAGCACTCCCCACGCTGCCCGTTCAGAGACATCTTGCAGTGTGGAGTTGTACAG  
GCCATGCTTGTCACAGTTG

**11778.1.contig**

GGGTTGGAGGGACTGGTCTTTATTTCAAAAAGCACTTGTCATATTCAGTATCAAAACAGTTGCACTATTG  
ATTTCTCTTTCTCCAATCGGCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCA  
GGATGTACACCTAACAGACCTCCTAGAAACCTTACCAGAAAATGGGGACTGGGTAGGGAAGGAACTTAA  
AGATCAACAACTGCCAGCCCACGGACTGCAGAGGCTGTACAGCCAGATGGGGTGGCCAGGGTGCCAC  
AAACCCAAAGCAAAGTTTCAAAAATAATAAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAG  
CACTGACTGATACAAAGCACAAATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGA  
TGAGATGAGTTTACATGGCTAAATCAGTGGCAAAACACAGTCTTCTTTCTTTCTTTCTTTCAAGGAGGCA  
GGAAAGCAATTAAGTGGTCACCTCAACATAAGGGGGACATGATCCATTCTGTAAGCAGTTGTGAAGGGG

**11778-2&30-2**

CAGGAACCGGAGCGCGAGCAGTAGCTGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAA  
GCGCAAGATCCAGTTCTGCAGCAGCAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGA  
AGTTGAGGGAGAAAGGCGGGCCCGGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCA  
GCTGGTTGAAGAAGAGCTGGACCGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCT  
GAAAAAGCTGCTGATGAGAGTGAGAGAGGTATGAAGGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAA  
GATGGAAGCTCCAGGAAATCCAACCAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAG  
AGGTGGCTCGTAAGTTGGTGATCATTGAAGGAGACTTGGAACGCACAGAGGAACGAGCTGAGCTGGCAGA  
GTCCCGTTGCCGAGAGATGGATGAGCAGATTAGACTGATGGACCAGAACCTGAAGTGTCTGAGTGC

**11782.1.contig**

ATCTACGTCATCAATCAGGCTGGAGACACCATGTTCAATCGAGCTAAGCTGCTCAATATTGGCTTTCAAGAG  
GCCTTGAAGGACTATGATTACAACTGCTTTGTGTTTCAGTGATGTGGACCTCATTCCGATGGACGACCGTAAT  
GCCTACAGGTGTTTTTCGCAGCCACGGCACATTTCTGTTGCAATGGACAAGTTCGGGTTTAGCCTGCCATA  
TGTTTCAGTATTTTGGAGGTGTCTCTGCTCTCAGTAAACAACAGTTTCTTGCCATCAATGGATTCCCTAATAAT  
TATTGGGGTTGGGGAGGAGAAGATGACGACATTTTAAACAGATTAGTTCATAAAGGCATGTCTATATCACGT  
CCAAATGCTGTAGTAGGGAGGTGTGCAATGATCCGGCATTCAAGAGACAAGAAAAATGAGCCCAATCCTCA  
GAGGTTTGACCGGATCGCACATACAAAGGAAACGATGCGCTTCGATGTTTTGAACTCACTTACCTACAAGG  
TGTTGGATGTCAGAGATACCCGTTATATACCCAAATCAC

**11782.2.contig**

CTAGACCTCTAATTAAGGACACAATCATGCTGGAGAATGAACAGTCTGACCCCGAGGGCCACAGCGAATT  
TTAGGGAAGGAGGCAAGAGGTGAGAAGGGAAAGGAAAGAAGGAAGGAGAACAATAAGAACTGGA  
GACGTTGGGTGGGTGAGGGAGTGTGGTGGAGGCTCGGAGAGATGGTAAACAAACCTGACTGCTATGAGTT  
TTCAACCCCATAGTCTAGGGCCATGAGGGCGTCAGTTCTTGGTGGCTGAGGGTCCTTCCACCCAGCCAC  
CTGGGGGAGTGGAGTGGGGAGTTCTGCCAGGTAAGCAGATGTTGTCTCCCAAGTTCTGACCCAGATGTC  
TGGCAGGATAACGCTGACCTGTTCCCTCAACAAGGGACCTGAAAGTAATTTGCTCTTTAC

**11783-1 & 2**

CCGAATTCAAGCGTCAACGATCCYTCCCTTACCATCAATCAATTGGCCACCAATGGTACTGAACCTACGAG  
TACACCGACTACGGCGGACTAATCTTCAACTCCTACATACTTCCCCCATTATTCCTAGAACCCAGGCGACCT  
GCGACTCCTTGACGTTGACAATCGAGTAGTACTCCCGATTGAAGCCCCCATTTCGTATAATAATTACATCACA  
AGACGTCTTGCACTCATGAGCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAGCC  
AAACCACTTTCACCGCTACACGACCGGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAACCAC  
AGTTTCATGCCCATCGTCCTAGAATTAATCCCTAAAAATCTTTGAAATAGGGCCCGTATTTACCCTATAGC  
ACCCCTCTACCCCTCTAG

**11786.1.contig**

GCTCTTCACACTTTTATTGTTAATTCTCTTCACATGGCAGATACAGAGCTGTCGTCTTGAAGACCACCACTGA  
CCAGGAAATGCCACTTTTACAAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAG  
CGTTGAAGGGTGACCAGCACATTTGCACATGCAAAAAAGGAGTGACCCCAAGGCCTCAACCACACTTCCCA  
GAGCTCACCATGGGCTGCAGGTGACTTGCCAGGTTTGGGGTTCGTGAGCTTTCCTTGCTGCTGCGGTGGG  
GAGGCCCTCAAGAACTGAGAGGCCGGGGTATGCTTCATGAGTGTTAACATTTACGGGACAAAAGCGCATCA  
TTAGGATAAGGAACAGCCACAGCACTTCATGCTTGTGAGGGTTAGCTGTAGGAGCGGGTGAAAGGATTCCA  
GTTTATGAAAATTTAAAGCAAACAACGGTTTTTGTAGCTGGGTGGGAAACAGGAAAACTGTGATGTCGGCCAAT  
GACCACCATTTTTCTGCCATGTGAAGGTCCCCATGAAACC

**11786.2.contig**

CAAGCGCTTGGCGTTTGGACCCAGTTCAGTGAGGTTCTTGGGTTTTGTGCCTTTGGGGATTTTGGTTTGAC  
CCAGGGGTCAGCCTTAGGAAGGTCTTCAGGAGGAGGCCGAGTTCCCCTTCAGTACCACCCCTCTCTCCCC  
ACTTTCCCTCTCCCGGCAACATCTCTGGGAATCAACAGCATATTGACACGTTGGAGCCGAGCCTGAACATG  
CCCCTCGGCCCCAGCACATGGAAAACCCCCTTCCTTGCCTAAGGTGTCTGAGTTTCTGGCTCTTGAGGCAT  
TTCCAGACTTGAAATTCTCATCAGTCCATTGCTCTTGAGTCTTTGCAGAGAACCTCAGATCAGGTGCACCTG  
GGAGAAAGACTTTGTCCCCACTTACAGATCTATCTCCTCCCTTGGGAAGGGCAGGGAATGGGGACGGTGT  
ATGGAGGGGAAGGGATCTCCTGCGCCCTTCATTGCCACACTTGGTGGGACCATGAACATCTTTAGTGTCTG  
AGCTTCTCAAATTACTGCAATAGGA

**13691.1&2**

AGCGTCAAATCAGAATGGAAAAGACTCAAAACCATCATCAACACCAAGATCAAAAGGACAAGRATCCTTCAAG  
AAACAGGAAAAAACTCCTAAAACACCAAAAGGACCTAGTTCTGTAGAAGACATTAAAGCAAAAATGCAAGCAA  
GTATAGAAAAAAGGTGGTTCTCTTCCCAAAGTGGAAGCCAAATTCATCAATTATGTGAAGAATTGCTTCCGGAT  
GACTGACCAAGAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTAAAGAAAATAGTTTAAACAATTTG  
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ACTTTCCCTACCGTGTTTGATAAATGTTGTCCAGGTTCTATTGCCAAGAATGTGTTGTCCAAAATGCCTGTTTA  
GTTTTTAAAGATGGAAGTCCACCCTTTGCTTGGTTTTAAGTATGTATGGAATGTTATGATAGGACATAGTAGTA  
GCGGTGGTCAGACATGGAAATGGTGGGSMGACAAAAATATACATGTGAAATAA

**13692.1&2**

TCCGAATTCGAAGCGAATTATGGACAAACGATTCCTTTTAGAGGATTACTTTTTCAATTTCCGTTTTAGTAAT  
CTAGGCTTTGCCTGTAAAGAATACAACGATGGATTTTAAATACTGTTTGTGGAATGTGTTTAAAGGATTGATT  
CTAGAACCTTTGTATATTTGATAGTATTTCTAACTTTCAATTTCTTTACTGTTTGCAGTTAATGTTTCATGTTCTGC  
TATGCAATCGTTTATATGCACGTTTCTTTAATTTTTTTAGATTTTCTGGATGTATAGTTTAAACAACAAAAAG  
TCTATTTAAAACTGTAGCAGTAGTTTACAGTTCTAGCAAAGAGGAAAGTTGTGGGGTTAACTTTGTATTTTC  
TTTCTTATAGAGGCTTCTAAAAAGGTATTTTTATATGTTCTTTTTAACAAATATTGTGTACAACCTTTAAACAT  
CAATGTTTGGATCAAAACAAGACCCAGCTTATTTTCTGC

**13693.2**

TGTGGTGGCGCGGGCTGAGGTGGAGGCCAGGACTCTGACCCTGCCCTGCCTTCAGCAAGGCCCCCGG  
CAGCGCCGGCCACTACGAAGTCCCGTGGGTTGAAAAATATAGGCCAGTAAAGCTGAATGAAATTGTCGGG  
AATGAAGACACCGTGAGCAGGCTAGAGGTCTTTGCAAGGGAAGGAAATGTGCCCAACATCATCATTGCGG  
GCCCTCCAGGAACCGGCAAGACCACAAGCATTCTGTGCTTGGCCCGGGCCCTGCTGGGCCCAGCACTCAA  
AGATGCCATGTTGGAAGTCAATGCTTCAAATGACAGGGGCATTGACGTTGTGAGGAATAAAATTTAAATGTT  
TGCTCAACAAAAAGTCACTCTTCCCAAAGGCCGACATAAGATCATCATTCTGGATGAAGCAGACAGCATGAC  
CGACGGAGCCCAGCAAGCCTTGAGGAGAACCATGGAAATCTACTCTAAAACCACTCGTTCGCCCTTGCTTG  
TAATGCTTCGATAAGATCATCGAGCC

**13696.1-13744.1**

CTTTGCAAAGCTTTTATTTTCATGTCTGCGGCATGGAATCCACCTGCACATGGCATCTTAGCTGTGAAGGAGA  
AAGCAGTGCACGAGAAGGAATGAGTGGGCGGAACCAACGGCCTCCACAAGCTGCCTTCCAGCAGCCTGC  
CAAGGCCATGGCAGAGAGAGACTGCAAACAAACACAAGCAAACAGAGTCTCTTCACAGCTGGAGTCTGAAA  
GCTCATAGTGGCATGTGTGAATCTGACAAAATTTAAAGTGTGCATAGTCCATTACATGCATAAAACACTAATA  
ATAATCCTGTTTACACGTGACTGCAGCAGGCAGGTCCAGCTCCACCACTGCCCTCCTGCCACATCACATCA  
AGTGCCATGGTTTAGAGGGTTTTTCATATGTAATTCCTTTATTCTGTAAAAGGTAACAAAATATACAGAACAA  
AACTTTCCCTTTTTAAACTAATGTTACAAATCTGTATTATCACTTGGATATAAATAGTATATAAGCTGATC

**13700.1**

CAAGGGATATATGTTGAGGGTACRGRGTGACACTGAACAGATCACAAAGCACGAGAAACATTAGTTCTCTC  
CCTCCCCAGCGTCTCCTTCGTCTCCCTGGTTTTCCGATGTCCACAGAGTGAGATTGTCCCTAAGTAACTGC  
ATGATCAGAGTGCTGKCTTTATAAGACTCTTCATTACAGCGTATCCAATTACAGCAATTGCTTCATCAAATGCCG  
TTTTTGCCAGGCTACAGGCCTTTTCAGGAGAGTTTAGAATCTCATAGTAAAAGACTGAGAAATTTAGTGCCA  
GACCAAGACGAATTGGGTGTGTAGGCTGCATTNCTTTCTTACTAATTTCAAATGCTTCCTGGTAAGCCTGCT  
GGGAGTTTGACACAAGTGGTTTGTGCTCCAGATGCCACTTCAGAAAGATACCTAAAATAATCTCCTT  
TCATTTTCAAAGTAGAACAC

**13700.2**

TCCGGAGCCGGGGTAGTCGCCGCCGCCGCCGCCGGTGCAGCCACTGCAGGCACCGCTGCCGCCGCCTG  
AGTAGTGGGCTTAGGAAGGAAGAGGTCATCTCGCTCGGAGCTTCGCTCGGAAGGGTCTTTGTTCCCTGCA  
GCCCTCCCACGGGAATGACAATGGATAAAAGTGAGCTGGTACAGAAAGCCAAACTCGCTGAGCAGGCTGA  
GCGATATGATGATATGGCTGCAGCCATGAAGGCAGTCACAGAACAGGGGCATGAACTCTCCAACGAAGAG  
AGAAATCTGCTCTCTGTTGCCTACAAGAATGTGGTAAGGCCGCCGCCGCTCTTCCTGGCGTGTCTCTCC  
AGCATTGAGCAGAAAACAGAGAGGAATGAGAAGAAGCAGCAGATGGGCAAAGAGTACCGTGAGAAGATAG  
AGGCAGAACTGCAGGACATCTGCAATGATGTTCTGGAGCTTGTGGACAAATATCTTATTCCAATGCTACAC  
AACCCAGAAA

**13701.1**

AAAAAGCAGCARGTTCAACACAAAATAGAAATCTCAAATGTAGGATAGAACAAAACCAAGTGTGTGAGGGG  
GGAAGCAACAGCAAAGGAAGAAATGAGATGTTGCAAAAAGATGGAGGAGGGTTCCTCTCCTCTGGG  
GACTGACTCAAACACTGATGTGGCAGTATACACCATTCAGAGTCAGGGGTGTTCACTTTTTTTGGGAGTA  
AGAAAAGGTGGGGATTAAGAAGACGTTTCTGGAGGCTTAGGGACCAAGGCTGGTCTCTTTCCCCCTCCCA  
ACCCCCTTGATCCCTTTCTCTGATCAGGGGAAAGGAGCTCGAATGAGGGAGGTAGAGTTGGAAGGGAAA  
GGATTCCAATTGACAGAATGGGACAGACTCCTTCCCA

**13701.2**

TGGCAATAGCACAGCCATCCAGGAGCTCTTCARGCGCATCTCGGAGCAGTTCACTGCCATGTTCCGCCGG  
AAGGCCTTCCTCCACTGGTACACAGGCCGAGGGCATGGACGAGATGGAGTTCACCGAGGCTGAGAGCAACA  
TGAACGACCTCGTCTCTGAGTATCAAGCAGTACCAGGATGCCACCGCAGAAGAGGAGGAGGATTTCCGGTG  
AGGAGGCCGAAGAGGAGGCCCTAAGGCAGAGCCCCATCACCTCAGGCTTCTCAGTTCCTTAGCCGTCTT  
ACTCAACTGCCCTTTCTCTCCCTCAGAATTTGTGTTTGCTGCCTCTATCTTGTTTTTGTCTTCTGCTG  
GGGGGTCTAGAACAGTGCCTGGCACATAGTAGGCGCTCAATAAATACTTGTTGNTGAATGTCTCT

**13702.2**

AGCTGGCGCTAGGGCTCGGTTGTGAAATACAGCGTRGTCAGCCCTTGCGCTCAGTGTAGAAACCCACGCC  
TGTAAGGTCGGTCTTCGTCCATCTGCTTTTTCTGAAATACACTAAGAGCAGCCACAAAAGTGAACCTCAA  
GGAAACCATAAAGCTTGGAGTGCCTTAATTTTAACAGTTTCCAATAAAACGGTTTACTACCT

**13704.2-13740.2**

GGAGATGAAGATGAGGAAGCTGAGTCAGCTACGGGCARGCGGGCAGCTGAAGATGATGAGGATGACGAT  
GTCGATACCAAGAAGCAGAAGACCGACGAGGATGACTAGACAGCAAAAAAGGAAAAGTTAAA

**13706.1**

GATGAAAATTAAATACTTAAATTAATCAAAAGGCACTACGATACCACCTAAAACCTACTGCCTCAGTGGCAGT  
AKGCTAAKGAAGATCAAGCTACAGSACATYATCTAATATGAATGTTAGCAATTACATAKCARGAAGCATGTTT  
GCTTTCCAGAAGACTATGGNACAATGGTCATTWGGGCCCAAGAGGATATTTGGCCNGGAAAGGATCAAGA  
TAGATNAANGTAAAG

**13706.2**

GAGTAGCAACGCAAAGCGCTTGGTATTGAGTCTGTGGGSGACTTCGGTTCCGGTCTCTGCAGCAGCCGTG  
ATCGCTTAGTGGAGTGCTTAGGGTAGTTGGCCAGGATGCCGAATATCAAATCTTCAGCAGGCAGCTCCCA  
CCAGGACTTATCTCASAAAATTGCTGACCGCCTGGGCCTGGAGCTAGGCAAGGTGGTACTAAGAAATTCA  
GCAACCAGGAGACCTGTGTGGAAATTGGTGAAAGTGATCCGTGGAGAGGATGTCTACATTGTTGAGAGTGG  
NTGTGGCGAAATCAATGACAATTTAATGGAGCTTTTGATCATGATTAATGCCTGCAAGATTGCTTCAGCCAG  
CCGGGTTACTGCAGTCATCCCATGCTTCCCTTATGCCCCGGCAGGATAAGAAAGATNAGAGCCGGGCCGC  
CAATCTCAGCCAAGCTTGGTGCAAATATGCTATCTGTAGCAGTGCAGATCATATTATCACCATGGACCTACA  
TGCTTCTCAAATTCANGGCTTTTT

**13707.3**

ATGCAAAAGGGGACACAGGGGGTTCAAAAATAAAAATTTCTCTTCCCCCTCCCCAAACCTGTACCCCAGCT  
CCCCGACCACAACCCCTTCTCCCCGGGAAAGCAAGAAGGAGCAGGTGTGGCATCTGCAGCTGGGA  
AGAGAGAGGCCGGGGAGGTGCCGAGCTCGGTGCTGGTCTCTTTCCAAATATAAATACGTGTGTCAGAACT  
GGAAAATCCTCCAGCACCCACCCCAAGCACTCTCCGTTTTCTGCCGGTGTTTGGAGAGGGGCGGNGGG  
CAGGGGCGCCAGGCACCGGCTGGCTGCGGTCTACTGCATCCGCTGGGTGTGCACCCCGCGA

**13710.2**

AGGTTGGAGAAGGTCATGCAGGTGCAGATTGTCCAGGSKCAGCCACAGGGTCAAGCCCAACAGGCCCAGA  
GTGGCACTGGACAGACCATGCAGGTGATGCAGCAGATCATCTAACACAGGAGAGATCCAGCAGATCCC  
GGTGCAGCTGAATGCCGGCCAGCTGCAGTATATCCGCTTAGCCAGCCTGTATCAGGCACTCAAGTTGTG  
CAGGGACAGATCCAGACACTTGCCACCAATGCTCAACAGATTACACAGACAGAGGTCCAGCAAGGACAGC  
AGCAGTTCAAGCCAGTTCACAAGATGGACAGCAGCTCTACCAGATCCAGCAAGTCACCATGCCTGCGGGC  
CANGACCTCGCCAGCCCATGTTTCATCCAGTCAAGCCAACCAGCCCTTCNACGGGCAGGCCCCCAGGTGA  
CCGGCGACTGAAGGGCCTGAGCTGGCAAGGCCAANGACACCCAACACAATTTTTGCCATACAGCCCCCAG  
GCAATGGGCACAGCCTTTCTTCCCAGAGGAC

**13710-1**

TGAGATTTATTGCATTTTCATGCAGCTTGAAGTCCATGCAAAGGRGACTAGCACAGTTTTTAATGCATTTAAAA  
AATAAAAGGGAGGTGGGCAGCAAACACACAAAGTCCTAGTTTCTGGGTCCCTGGGAGAAAAGAGTGTGG  
CAATGAATCCACCCACTCTCCACAGGGAATAAATCTGTCTCTTAAATGCAAAGAATGTTTCCATGGCCTCTG  
GATGCAAATACACAGAGCTCTGGGGTCAGAGCAAGGGATGGGGAGAGGACCACGAGTGAAAAAGCAGCTA  
CACACATTCACCTAATTCCATCTGAGGGCAAGAACAACGTGGCAAGTCTTGGGGGTAGCAGCTGTT

**13711.1**

TCCAGACATGCTCCTGTCTAGGCGGGGAGCAGGAACCAGACCTGCTATGGGAAGCAGAAAGAGTTAAGG  
GAAGGTTTCCTTTTCATTCTGTTCTTCTCTTTTGCTTTTGAACAGTTTTTAAATATACTAATAGCTAAGTCAT  
TTGCCAGCCAGGTCCCGGTGAACAGTAGAGAACAAGGAGCTTGCTAAGAATTAATTTTGCTGTTTTTACCC  
CATTCAAACAGAGCTGCCCTGTTCCCTGATGGAGTTCATTCTGCCAGGGCACGGCTGAGTAACACGAAG  
CCATTCAAGAAAGGCGGGTGTGAAATCACTGCCACCCCATGGACAGACCCCTCACTCTTCTTCTTAGCCG  
CAGCGCTACTTAATAAATATATTTATACTTTGAAATTATGATAACCGATTTTTCCCATGCGGCATCCTAAGGG  
CACTTGCCAGCTCTTATCCGGACAGTCAAGCACTGTTGTTGGACAACAGATAAAGGAAAAGAAAAAGAAGA  
AAACAACCGCAACTTCTGT

**"REPLACEMENT SHEETS"**

**13711.2**

TGAGACGGACCACTGGCCTGGTCCCCCTCATKTGCTGTCGTAGGACCTGACATGAAACGCAGATCTAGT  
GGCAGAGAGGAAGATGATGAGGAACTTCTGAGACGTCGGCAGCTTCAAGAAGAGCAATTAATGAAGCTTAA  
CTCAGGCCTGGGACAGTTGATCTTGAAAAGAAGAGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTTA  
GCCAGTCGCTACGATTCTCCCATCAACTCAGCTTCACATATTCATCATCTAAACTGCATCTCTCCCTGGC  
TATGGAAGAAATGGGCTTACCGGCCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCAG  
CGGGGGAGTGCGAGATTACCAGACACTTCCAGATGGCCACATGCCTGCAATGAGAATGGACCGAGGAGTG  
TCTATGCCCAACATGTTGGAACCAAAGATATTTCCATATGAAATGCTCATGTTGACCAACAGAGGGCCGAAA  
CCAAATCTCAGAGAGGTGGACAGAA

**13713.1&2**

TCACTTTATTTTTCTTGTATAAAAACCCTATGTTGTAGCCACAGCTGGAGCCTGAGTCCGCTGCACGGAGAC  
TCTGGTGTGGGTCTTGACGAGGTGGTCAGTGAACCTCTGATAGGGAGACTTGGTGAATACAGTCTCCTTCC  
AGAGTTCGGGGGTGAGGTAGCTGTAGGTCTTAGAAATGGCATCAAAGGTGGCCTTGGCGAAGTTGCCAG  
GGTGGCAGTGCAGCCCCGGGCTGAGGTGTAGCAGTCATCGATACCAGCCATCATGAG

**13715.4**

CTGGAATATAGACCCGTGATCGACAAAACCTTTGAACGAGGCTGACTGTGCCACCGTCCCGCCAGCCATTCC  
CTCCTACTGATGAGACAAGATGTGGTGTGACAGAATCAGCTTTTGAATTATGTATAATAGCTCATGCATGT  
GTCCATGTCATAACTGTCTTCATACGCTTCTGCACTCTGGGGAAGAAGGAGTACATTGAAGGGAGATTGGC  
ACCTAGTGGCTGGGAGCTTGCCAGGAACCCAGTGGCCAGGGAGCGTGGCACTTACCTTTGTCCCTTGCTT  
CATTCTTGTGAGATGATAAACTGGGCACAGCTCTTAAATAAAATATAAATGAACA

**13717.1&2**

TGAATGGGGAGGAGCTGACCCAGGAAATGGAGCTTGNGGAGACCAGGCCTGCAGGGGATGGAACCTTCC  
AGAAGTGGGCATCTGTGGTGGTGCCTCTTGGGAAGGAGCAGAAGTACACATGCCATGTGGAACATGAGGG  
GCTGCCTGAGCCCCTCACCTGAGATGGGGCAAGGAGGAGCCTCCTTCATCCACCAAGACTAACACAGTA  
ATCATTGCTGTTCCGGTTGTCCTTGGAGCTGTGGTCATCCTTGGAGCTGTGATGGCTTTTGTGATGAAGAG  
GAGGAGAAACACAGGTGGAAAAGGAGGGGACTATGCTCTGGCTCCAGGCTCCCAGAGCTCTGATATGTCT  
CTCCCAGATTGTAAAGTGTGAAGACAGCTGCCTGGTGTGGACTTGGTGACAGACAATGTCTTCACACATCT  
CCTGTGACATCCAGAGACCTCAGTTCTCTTTAGTCAAGTGTCTGATGTTCCCTGTGAGTCTGCGGGCTCAA  
GTGAAGAACTGTGGAGCCCAGTCCACCCCTGCACACCAGGACCCTATCCCTGCACTGCCCTGTGTTCCCTT  
CCACAGCCAACCTTGCTGCTCCAGCCAAACATTGGTGGACATCTGCAGCCTGTCAGCTCCATGCTACCCTG  
ACCTTCAACTCCTCACTTCCACACTGAGAATAATAATTTGAATGTGGGTGGCTGGAGAGATGGCTCAGCGC  
TGACTGCTCTTCAAAGGTCCTGAGTTCAAATCCAGCAACCACATGGTGGCTCACAACCATCTGTAATGG  
GATCTAATACCCTCTTCTGCAGTGTCTGAAGACASCTACAGTGTACTTACATATAATAATAAATAAG

**13719.1&2**

GGCCGGGCGCGCGCGCCCCGCCACACGCACGCCGGGCGTGCCAGTTTATAAAGGGAGAGAGCAAGCA  
GCGAGTCTTGAAGCTCTGTTTGGTGCTTTGGATCCATTTCCATCGGTCCTTACAGCCGCTCGTCAGACTCC  
AGCAGCCAAGATGGTGAAGCAGATCGAGAGCAAGACTGCTTTTCAGGAAGCCTTGGACGCTGCAGGTGAT  
AACTTGTAGTAGTTGACTTCTCAGCCACGTGGTGTGGGCCTTGCAAATGATCAAGCCTTTCTTTCATTCC  
CTCTCTGAAAAGTATTCCAACGTGATATTCCTTGAAGTAGATGTGGATGACTGTCAGGATGTTGCTTCAGAG  
TGTGAAGTCAAATGCATGCCAACATTCCAGTTTTTTAAGAAGGGACAAAAGGTGGGTGAATTTTCTGGAGCC  
AATAAGGAAAAGCTTGAAGCCACCATTGAATTAAGTCTAATCATGTTTTCTGAAAATATAACCAGCCATTG  
GCTATTTAAACTTGAATTTTTTTAATTTACAAAATATAAAATATGAAGACATAAACCCMGTGCCATCTGC  
GTGACAATAAACATTAATGCTAACACTT

**13721.1**

TCACATAAGAAATTTAAGCAAGTTACRCTATCTTAAAAACACAACGAATGCATTTTAATAGAGAAACCCTTC  
CCTCCCTCCACCTCCCTCCCCACCCTCCTCATGAATTAAGAATCTAAGAGAAGAAGTAACCATAAAACCAA  
GTTTTGTGGAATCCATCATCCAGAGTGCTTACATGGTGATTAGGTTAATATTGCCTTCTTACAAAATTTCTAT  
TTTAAAAAAATTATAACCTTGATTGCTTATTACAAAAAAATTCAGTACAAAAGTTCAATATATTGAAAAATGCT  
TTTCCCTCCCTCACAGCACCGTTTTATATATAGCAGAGAATAATGAAGAGATTGCTAGTCTAGATGGGGCA  
ATCTTCAAATTACACCAAGACGCACAGTGGTTTATTTACCCTCCCCTTCTCATAAG

**13721.2**

GGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTRRAGAAAAAGACAACCTCTCGTCGCATGCTGACAGACA  
AAGAGAGAGAGATGGCGGAAATAAGGGATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGAT  
GTAAAGTTAGCCCTGGACATGGAAATCAGTGCTTACAGGAACTCTTAGAAGGCGAAGAAGAGAGGTTGAA  
GCTGTCTCCAAGCCCTTCTTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACCGTACAAC  
AGAGGAAAGCGGAAGAGGGTTGATGTGGAAGAATCAGAGGCGAAGTAGTAGTGTAGCATCTCTCATTCC  
GCCTCAACCACTGGAATGTTTGCATCGAAGAAATTGATGTTGATGGGAAATTTATCCCGCTTGAAGAACAC  
TTCTGAACAGGATCAACCAATGGGAAGGCTTGGGAGATGATCAGAAAAATTGGAGACACATCAGTCAGTTA  
TAAATATACCTCAA

**13723.1**

CATGGGTTTCACCAGGTTGGCCAGGCTGCTCTTGAACTSCTGACCTCAGGTGATCCACCCGCCTCGGCCT  
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGCCCGGCCCCCAAAGCTGTTTCTTTGTCTTTAGCG  
TAAAGCTCTCCTGCCATGCAGTATCTACATAACTGACGTGACTGCCAGCAAGCTCAGTCACTCCGTGGTCTT  
TTTCTCTTTCCAGTTCTTCTCTCTCTTCAAGTTCTGCCTCAGTGAAAGCTGCAGGTCCCAGTTAAGTGAT  
CAGGTGAGGGTTCTTTGAACCTGGTTCTATCAGTCGAATTAATCCTTCATGATGG



**13723.2**

GATGTGTTGGACCCTCTGTGTCAAAAAAACCTCACAAAGAATCCCCTGCTCATTACAGAAGAAGATGCATT  
TAAATATGGGTTATTTTCAACTTTTTATCTGAGGACAAGTATCCATTAATTATTGTGTCAGAAGAGATTGAAT  
ACCTGCTTAAGAAGCTTACAGAAGCTATGGGAGGAGGTTGGCAGCAAGAACAATTTGAACATTATAAAATCA  
ACTTTGATGACAGTAAAAATGGCCTTTCTGCATGGGAACCTATTGAGCTTATTGGAAATGGACAGTTTAGCA  
AAGGCATGGACCGGCAGACTGTGTCTATGGCAATTAATGAAGTCTTTAATGAACCTATATTAGATGTGTTAA  
AGCAGGGTTACATGATGAAAAAGGGCCACAGACGGAAAAACTGGACTGAAAGATGGTTTTGTACTAAACCC  
AACATAATTTCTTACTATGTGAGTGAGGATCTGAAGGATAAGAAAGGAGACATTCTCTTGGATGAAAATTGC  
TGTGTAGAAGTCCTTGCCTGACAAAAGATGGAAAGAAATGCCTTTT

**13725.1**

GACTGGTTCTTTATTTCAAAAAGACACTTGTCAATATTCAGTRTCAAAACAGTTGCACTATTGATTTCTCTTTC  
TCCCAATCGGCCCCAAAGAGACCACATAAAAGGAGAGTACATTTTAAGCCAATAAGCTGCAGGATGTACAC  
CTAACAGACCTCCTAGAAACCTTACCAGAAAATGGGACTGGGTAGGGAAGGAACTTAAAAGATCAACAA  
ACTGCCAGCCCACGGACTGCAGAGGCTGTCACAGCCAGATGGGGTGGCCAGGGTGCCACAAACCCAAAG  
CAAAGTTTCAAATAATATAAAATTTAAAAAGTTTTGTACATAAGCTATTCAAGATTTCTCCAGCACTGACTGA  
TACAAAGCACAATTGAGATGGCACTTCTAGAGACAGCAGCTTCAAACCCAGAAAAGGGTGATGAGATGAAG  
TTTCACATGGCTAAATCAGTGGCAAAAACACAGTCTTCTTTCTTTCTTTCTTTCAAGGANGCAGGAAAGCAAT  
TAAGTGGTCACCTTAACATAAGGGGGAC

**13725.2**

TGGGTGGGCACCATGGCTGGGATCACCACCATCGAGGCGGTGAAGCGCAAGATCCAGGTTCTGCAGCAG  
CAGGCAGATGATGCAGAGGAGCGAGCTGAGCGCCTCCAGCGAGAAGTTGAGGGAGAAAGGCGGGCCCG  
GGAACAGGCTGAGGCTGAGGTGGCCTCCTTGAACCGTAGGATCCAGCTGGTTGAAGAAGAGCTGGACCGT  
GCTCAGGAGCGCCTGGCCACTGCCCTGCAAAAGCTGGAAGAAGCTGAAAAAGCTGCTGATGAGAGTGAGA  
GAGGTATGAAGTTATTGAAAACCGGGCCTTAAAGATGAAGAAAAGATGGAACCTCAGGAAATCCAACCTC  
AAAGAAGCTAAGCACATTGCAGAAGAGGCAGATAGGAAGTATGAAGAGGTGGCTCGTAAGTTGGTGATCAT  
TGAAGGAGACTTGGAACCGCACAGAAGGAACGAGCTTGAGCTTGGCAAAAGTCCCGTTGCCCAGAGATGG  
GATGAACCAGATTAGACTGATGGACCANAACC

**13726.1&2**

AGGGGCGNGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCG  
CCCCGAGAGTGACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCT  
CCTTGTCGCCTGCATTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATC  
AACGAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCG  
TGCACCTCGGGCACTCAAAGAGATTGCGAAATTTGCCATGAAGGAGATGGGAACCTCAGATGTGCGCATTG  
ACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGGTGTGCGGC  
TGTCCAGAAAACGTAATGAGGATGAAGATTCACCAATAAGCTATATACTTTGGTTACCTATGTACCTGTTAC  
CACTTTCAAAAATCTACAGACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATA  
AAAT

**13727.1**

TCGGGAGCCACACTTGGCCCTCTTCCTCTCCAAAGSGCCAGAACCCTCCTTCTCTTTGGAGAATGGGGAGGC  
CTCTTGGAGACACAGAGGGTTTCACCTTGGATGACCTCTAGAGAAATTGCCCAAGAAGCCCACCTTCTGGT  
CCCAACCTGCAGACCCACAGCAGTCAGTTGGTCAGGCCCTGCTGTAGAAGGTCACCTGGCTCCATTGCC  
TGCTTCCAACCAATGGGCAGGAGAGAAGGCCCTTTATTTCTCGCCCACCCATTCTCCTGTACCAGCACCTC  
CGTTTTTCAGTCAGTGTTGTCCAGCAACGGTACCGTTTACACAGTCACCTCAGACACACCATTTCACCTCCCT  
TGCCAAGCTGTTAGCCTTAGAGTGATTGCAGTGAACACTGTTTACACACCGTGAATCCATTCCCATCAGTCC  
ATTCCAGTTGGCACCAGCCTGAACCATTTGGTACCTGGTGTTAACTGGAGTCCTGTTTACAAGGTGGAGTC  
GGGGCTTGCTGACTTCTCTTCATTTGAGGGCAC

**13727.2**

ACCTAGACAGAAGGTGGGTGAGGGAGGACTGGTAGGAGGCTGAGGCAATTCCTTGGTAGTTTGTCTGAA  
ACCCTACTGGAGAAGTCAGCATGAGGCACCTACTGAGAGAAGTGCCCAAGAACTGCTGACTGCATCTGTTA  
AGAGTTAACAGTAAAGAGGTAGAAGTGTTTCTGAATCAGAGTGGAAGCGTCTCAAGGGTCCCACAGTGG  
AGGTCCCTGAGCTACCTCCCTTCCGTGAGTGGGAAGAGTGAAGCCCATGAAGAACTGAGATGAAGCAAGG  
ATGGGGTTCTGGGCTCCAGGCAAGGGCTGTGCTCTCTGCAGCAGGGAGCCCCACGAGTCAGAAGAAAA  
GAACTAATCATTTGTTGCAAGAAACCTTGCCCGGATACTAGCGGAAACTGGAGGCGGNGGTGGGGGCAC  
AGGAAAGTGGAAGTGATTTGATGGAGAGCAGAGAAGCCTATGCACAGTGGCCGAGTCCACTTGTAAGTG

**13728.1&2**

TTCAAGCAATTGTAACAAGTATATGTAGATTAGAGTGAGCAAAATCATATACAATTTTCATTTCCAGTTGCTAT  
TTTCCAAATTGTTCTGTAATGTCGTTAAAATTACTTAAAAATTAACAAAGCCAAAAATTATATTTATGACAAGA  
AAGCCATCCCTACATTAATCTTACTTTTCCACTCACCGGCCCATCTCCTTCCTCTTTTTCTAACTATGCCAT  
TAAAACTGTTCTACTGGGCGGGCGTGTGGCTCATGCCTGTAATCCCAGCATTTTGGGAGGCCAAGGCAG  
GCGGATCATGAGGTCAAGAGATTGAGACCATCCTGGCCAACATGGTGAAACCCCGCCTCGACTAAGAATAC  
AAAAATTAGCTGGGCATGGTGGCGCATGCCTGTAGTCTCAGCTACTCGGGAGGCTGAGGCAGAAGAATCG  
CTTGAACCCGGGAGGCAGAGGATGCAGTGAGCCCCGATCGCGCCACTGCACTCTAGCCTGGGCGACAGA  
CTGAGACTCTGCTC

**13731.1&2**

TGTGCCAGTCTACAGGCCTATCAGCAGCGACTCCTTCAGCAACAGATGGGGTCCCCTGTTTCAGCCCAACC  
CCATGAGCCCCCAGCAGCATATGCTCCCAAATCAGGCCAGTCCCCACACCTACAAGGCCAGCAGATCCC  
TAATTCTCTCTCCAATCAAGTGCGCTCTCCCCAGCCTGTCCCTTCTCCACGGCCACAGTCCCAGCCCCC  
ACTCCAGTCCTTCCCCAAGGATGCAGCCTCAGCCTTCTCCACACCACGTTTCCCCACAGACAAGTTCCCCA  
CATCCTGGACTGGTAGTTGCCCAGGCCAACCCCATGGAACAAGGGCATTGTCAGCC

**"REPLACEMENT SHEETS"**

**13734.1&2**

TGTA AAAA ACTTGT TTTTAATTTTGTATAAAATAAAGGTGGTCCATGCCACGGGGGCTGTAGGAAATCCAAG  
CAGACCAGCTGGGGTGGGGGGATGTAGCCTACCTCGGGGACTGTCTGTCTCCTCAAACGGGCTGAGAAG  
GCCCCGTAGGGGGCCAGGTCCACAGAGAGGCCTGGGATACTCCCCAACCCGAGGGGCAGACTGGGCA  
GTGGGGAGCCCCCATCGTGCCCCAGAGGTGGCCACAGGCTGAAGGAGGGGGCCTGAGGCACCGCAGCCT  
GCAACCCCCAGGGCTGCAGTCCACTAACTTTTTACAGAATAAAAGGAACATGGGGATGGGGAAAAAAGCAC  
CAGGTCAGGCAGGGCCCCGAGGGCCCCAGATCCCAGGAGGGCCAGGACTCAGGATGCCAGCACCACCCTA  
GCAGCTCCACAGCTCCTGGCACAGGAGGCCGCCACGGATTGGCACAGGCCGCTGCTGGCCATCACGCC  
ACATTTGGAGAACTTGTCCCGACAGAGGTCAGCTCGGAGGAGCTCCTCGTGGGCACACACTGTACGAACA  
CAGATCTCCTTGTTAATGACGTACACACGGCGGAGGCTGCGGGGACAGGGCACGGGAGGTCTCAGCCCC  
ACTT

**13736.2**

ATGGCTGCTGGATTTAGGTGGTAATAGGGGCTGTGGGCCATAAATCTGAAGCCTTGAGAACCTTGGGTCTG  
GAGAGCCATGAAGAGGGAAGGAAAAGAGGGCAAGTCCTGAACCTAACCAATGACCTGATGGATTGCTCGA  
CCAAGACACAGAAGTGAAGTCTGTGTCTGTGCACTTCCCACAGACTGGAGTTTTTGGTGCTGAATAGAGCC  
AGTTGCTAAAAAATTGGGGGTTTGGTGAAGAAATCTGATTGTTGTGTGATTCAATGTGTGATTTTAAAAATA  
AACAGCAACAACAATAAAAACCCCTGACTGGCTGTTTTTCCCTGTATTCTTTACAACTATTTTTTGACCCTCT  
GAAAATTATTATACTTACCTAAATGGAAGACTGCTGTGTTTGTGGAAATTTTGTAAATTTTTAATTTATTTAT  
TCTCTCTCTTTTATTTTGCCTGCAGAATCCGTTGAGAGACTAATAAGGCTTAATATTTAATTGATTTGTTA  
ATATGTATATAAAT

**13744.2-13696.2**

GGCATGCGAGCGCACTCGGCGGACGCAAGGGCGGGCGGGGAGCACACGGAGCACTGCAGGCGCCGGGTT  
GGGACAGCGTCTTCGCTGCTGCTGGATAGTCGTGTTTTCGGGGATCGAGGATACTCACCAGAAACCGAAA  
ATGCCGAAACCAATCAATGTCCGAGTTACCACCATGGATGCAGAGCTGGAGTTTGCAATCCAGCCAAATAC  
AACTGGAAAACAGCTTTTTGATCAGGTGGTAAAGACTATCGGCCTCCGGGAAGTGTGGTACTTTGGCCTCC  
ACTATGTGGATAATAAAGGATTTCTACCTGGCTGAAGCTGGATAAGAAGGTGTCTGCCCAGGAGGTCAGG  
AAGGAGAATCCCCTCCAGTTCAAGTTCCGGGGCCAAaGTTCTACCCTGAAGATGTGGCTGAGGAGCTCATCC  
AGGACATCACCCAGAACTTTTCTTCTTCAAGTGAAGGAAGGAATCCTTAGCGATGAGATCTACTGCCCCC  
CTTGARACTGCCGTGCTCTTGGGGTCCTACGCTTGTGCATGCCAAGTTTGGGGACTACCACCAAGAAG

**13746.1&2-13720.1&2**

GAAGGAGTCGGGATACTCAGCATTGATGCACCCCAATTTCAAAGCGGCATTCTTCGGCAGGTCTCTGGGAC  
AATCTCTAGGGTCACTACCTGGAACTCGTTAGGGTACAAGTGAATGCTGAAAGGAAAGAACACCTGCAGA  
ACCGGACAGAAATTCACCCCGGCGATCAGCTGATTGATCTCGGTGACACAGAGTCATGGCTAAAGATGAC  
GAGGACGTTGTCAATTCCCTGGGCTTTTTCGAAGTGAGTCCAGCAGCAGTCTGAGGTATTTCGGGCCGGTTAT  
GCACCTGGACCACCAGCACCAGCTCCCGGGGGGCCAGGTGCCAGCCTTATCTACATTCCTCAGGGTCTG  
ATCAAAGTTCAGCTGGTACACCAGGGACCGGTACCGCAGCGTCAGGTTGTCCGCTCGGGCTGGGGGACC  
GCCGGGACCAGGGAAGCCGCCGACACGTTGGAGACCCTGCGGATGCCACAGCCACAGAGGGGTGGTC  
CCCACCGCGGCCGCCGCCGACCCCGCGCGGGTTCCGGCTCCAGCAACGGTGGGGCGAGGGCCTCGTTCT  
TCCTTTGTCGCCCATTTGCTGCTCCAGAGGACGAAGCCGCAGGCGGCCACCACGAGCGTCAGGATTAGCAC  
CTTCCGTTTGTAGATGCGGAACCTCATGGTCTCCAGGGCCGGGAGCGCAGCTACAGCTCGAGCGTCGGCG  
CCGCCGCTAGGAGCCGCGGCTCGGCTTCGTCTCCGTCTCCTTCCATTACGACACACGGGTCCCGGAAAAAG  
CTCAGCCSCGGTCCCAACCGCACCCCTAGCTTCGTTACCTGCGCCTCGCTTG

**"REPLACEMENT SHEETS"**

**14347.1**

CAGATTTTATTTGCAGTCGTCAGTGGGGCCGTTTCTTGCTGCTTATTTGTCTGCTAGCCTGCTCTTCCAGC  
TGCATGGCCAGGCGCAAGGCCTTGATGACATCTCGCAGGGCTGAGAAATGCTTGGCTTGCTGGGCCAGAG  
CAGATTCCGCTTTGTTACAAAGGTCTCCAGGTCATAGTCTGGCTGCTCGGTCATCTCAGAGAGCTCAAGC  
CAGTCTGGTCCTTGCTGTATGATCTCCTTGAGCTCTTCCATAGCCTTCTCCTCCAGCTCCCTGATCTGAGTC  
ATGGCTTCGTTAAAGCTGGACATCTGGGAAGACAGTTCCTCCTCTTCCCTTGATAAATTGCCTGGAATCAGC  
GCCCCGTTAGAGCAGGCTTCCATCTCTTCTGTTTCCATTTGAATCAACTGCTCTCCACTGGGCCCACTGTG  
GGGGCTCAGCTCCTTGACCCTGCTGCATATCTTAAGGGTGTTAAAGGATATTACAGGAGCTTATGCCTG  
GT

**14347.2**

CTCCTCTTGGTACATGAACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTT  
GACTTTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTTACAGCAAGGCCACTGGTACAGACA  
ATCTTTGAAGGTGGAAAAGCAACTTGTTTTGCATATGGCCAGACAGGAAGTGGCAAGACACATACTATGGG  
CGGAGACCTCTCTGGGAAAGCCAGAATGCATCCAAAGGGATCTATGCCATGGCCTTCCGGGACGTCTTC  
TTCTGAAGAATCAACCCTGCTACCGGAAGTTGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATG  
GGAAGCTGTTTGACCTGCTCAACAAGAAGGCCAAGCTTGCGCGTGCTGGAAGACGGCAAGCAACAGGTGC  
AAGTGGTGGGGGCTTGCGAGGAACATCTGGNTAACTCTGCTTGATGATGGCANTCAAGATGATCGACATGG  
GCAGCGCCTGCAGA

**14348.2&14350.1&2**

TCCCGAATTCAAGCGACAAATTGGAWAGTGAAATGGAAGATGCCTATCATGAACATCAGGCCAAATCTTTTG  
CGCCAAGATCTGATGAGACGACAGGAAGAATTAAGACGCATGGAAGAAGTTTACAAATCAAGAAATGCAGAA  
ACGTAAAGAAATGCAATTGAGGCAAGAGGAGGAACGACGTAGAAGAGAGGAAGAGATGATGATTCGTCAA  
CGTGAGATGGAAGAACAAATGAGGCGCCAAAGAGAGGAAGTTACAGCCGAATGGGCTACATGGATCCAC  
GGGAAAGAGACATGCGAATGGGTGGCGGAGGAGCAATGAACATGGGAGATCCCTATGGTTCAGGAGGCC  
AGAAATTTCCACCTCTAGGAGGTGGTGGTGGCATAGGTTATGAAGCTAATCCTGGCGTTCCACCAGCAACC  
ATGAGTGGTTCATGATGGGAAGTGACATGCGTACTGAGCGCTTTGGGCAGGGAGGTGCGGGGCCTGTG  
GGTGGACAGGGTCTAGAGGAATGGGGCCTGGAAGTCCAGCAGGATATGGTAGAGGGAGAGAAGAGTAC  
GAAGGC

**14349.1&2**

TTCGTGAAGACCCTGACTGGTAAGACCATCACTCTCGAAGTGGAGCCCGAGTGACACCATTGAGAATGTCA  
AGGCAAAGATCCAAGACAAGGAAGGCATCCCTCCTGACCAGCAKAGGTTGATCTTTGCTGGGAAACAGCTG  
GAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGTCCGTCTCAG  
AGGTGGGATGCAAATCTTCGTGAAGACCCTGACTGGTAAGACCATCACCTCGAGGTGGAGCCCAGTGAC  
ACCATCGAGAATGTCAAGGCAAAGATCCAAGATAAGGAAGGCATCCCTCCTGATCAGCAGAGGTTGATCTT  
TGCTGGGAAACAGCTGGAAGATGGACGCACCCTGTCTGACTACAACATCCAGAAAGAGTCCACTCTGCACT  
TGGTCCTGCGCTTGAGGGGGGGGTGTCTAAGTTTCCCTTTTAAGGTTTCAACAAATTTCAATTGCACTTTCCT  
TTCAATAAAGTTGTTGCATTC

**"REPLACEMENT SHEETS"**

**14352.1&2**

GCGCGGGTGCGTGGGCCACTGGGTGACCGACTTAGCCTGGCCAGACTCTCAGCACCTGGAAGCGCCCCG  
AGAGTGACAGCGTGAGGCTGGGAGGGAGGACTTGGCTTGAGCTTGTTAACTCTGCTCTGAGCCTCCTTG  
TCGCTGCATTTAGATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAACGA  
AGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTCAAGAAGCGTGCAC  
CTCGGGCACTCAAAGAGATTTCGGAAATTTGCCATGAAGGAGATGGGAACTCCAGATGTGCGCATTGACACC  
AGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCA  
GAAACGTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTT  
CAAAAATCTACAGACAGTCAATGTGGATGAGAACTAATCGCTGATCGT

**14353.1**

AATTCTTTATTTAAATCAACAACTCATCTTCTCAAGCCCCAGACCATGGTAGGCAGCCCTCCCTCTCCAT  
CCCCTCACCCACCCCTTAGCCACAGTGAAGGGAATGGAAAATGAGAAGCCACGAGGGGCCCTGCCAGG  
GAAGGCTGCCCCAGATGTGTGGTGAGCACAGTCAGTGCAGCTGTGGCTGGGGCAGCAGCTGCCACAGGC  
TCCTCCCTATAAATTAAGTTCCTGCAGCCACAGCTGTGGGAGAAGCATACTTGTAGAAGCAAGGCCAGTCC  
AGCATCAGAAGGCAGAGGCAGCATCAGTGACTCCAGCCATGGAATGAACGGAGGACACAGAGCTCAGAG  
ACAGAACAGGCCAGGGGGAAGAAGGAGAGACAGAATAGGCCAGGGCATGGCGGTGAGGGA

**14353.2**

TGATGAATCTGGGTGGGCTGGCAGTAGCCCGAGATGATGGGCTCTTCTCTGGGGATCCCAACTGGTTCCC  
TAAGAAATCCAAGGAGAATCCTCGGAACCTCTCGGATAACCAGCTGCAAGAGGGCAAGAACGTGATCGGGT  
TACAGATGGGCACCAACCGCGGGGCGTCTCANGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCC  
TCTGATCCCACCCAGGCCCTTGCCCTGCCCTCCACGAATGGTTAATATATATGTAGATATATATTTTAGC  
AGTGACATTCCCAGAGAGCCCCAGAGCTCTCAAGCTCCTTTCTGTGAGGGTGGGGGGTTCAAGCCTGTCC  
TGTCACCTCTGAAGTGCCTGCTGGCATCCTCTCCCCATGCTTACTAATACATTCCCTTCCCCATAGCC

**17182.1&2**

AGCGGAGCTCCCTCCCCTGGTGGCTACAACCCACACACGCCAGGCTCAGGCATCGAGCAGAACTCCAGC  
GACTGGGTAACCACTGACATTCAGGTGAAGGTGCGGGACACCTACCTGGATACACAGGTGGTGGGACAGA  
CAGGTGTCATCCGCAGTGTACGGGGGGCATGTGCTCTGTGTACCTGAAGGACAGTGAGAAGGTTGTCAG  
CATTTCCAGTGAGCACCTGGAGCCTATCACCCCCACCAAGAACAACAAGGTGAAAGTGATCCTGGGCGAG  
GATCGGGAAGCCACGGGCGTCTACTGAGCATTGATGGTGAGGATGGCATTGTCCGTATGGACCTTGATG  
AGCAGCTCAAGATCCTCAACCTCCGCTTCTGGGGAAGCTCCTGGAAGCCTGAAGCAGGCAGGGCCGGTG  
GACTTCGTGCGGATGAAGAGTGATCCTCCTTCCCTTCCCTGGCCCTTGGCTGTGACACAAGATCCTCCTGCAG  
GGCTAGGCGGATTGTTCTGGATTTCTTTTGTTCCTTTAGGTTTCCATCTTTCCCTCCCTGGTGCTCA  
TTGGAATCTGAGTAGAGTCTGGGGGAGGGTCCCCACCTTCTGTACCTCCTCCCCACAGCTTGCTTTTGT  
GTACCGTCTTTCAATAAAAAGAAGCTGTTTGGTCTA

17183.2

GGTTCACAGCACTGCTGCTTGTGTGTTGCCGGCCAGGAATTCCAGGCTCACAAGGCTATCTTAGCAGCTCG  
TTCTCCGGTTTTTAGTGCCATGTTTGAACATGAAATGGAGGAGAGCAAAAAGAATCGAGTTGAAATCAATGA  
TGTGGAGCCTGAAGTTTTTAAGGAAATGATGTGCTTCATTTACACGGGGAAGGCTCCAAACCTCGACAAAAT  
GGCTGATGATTTGCTGGCAGCTGCTGACAAGTATGCCCTGGAGCGCTTAAAGGTCATGTGTGAGGATGCC  
CTCTGCAGTAACCTGTCCGTGGAGAACGCTGCAGAAATTCTCATCCTGGCCGACCTCCACAGTGCGAGATCA  
GTTGAAAACCTCAGGCAGTGGATTTTCACTCAACTATCATGCTTCGGATGTCTTGGAGACCTCTTGGG

17186.1&2

TCGTAGCCATTTTTCTGCTTCTTTGGAGAATGACGCCACACTGACTGCTCATTGTCGTTGGTTCCATGCCAA  
TTGGTGAAATAGAACCTCATCCGGTAGTGAGCCGGAGGGACATCTTGTCAACGGTGATGGTGCGATT  
TGGAGCATACCAGAGCTTGGTGTCTCGCCATACAGGGCAAAGAGGTTGTGACAAAGAGGAGAGATACGG  
CATGCCTGTGCAGCCCTGATGCACAGTTCCTCTGCTGTGTACTCTCCACTGCCAGCCGGAGGGGCTCCC  
TGTCGACAGATAGAAGATCACTTCCACCCCTGGCTTG

17187.1&2

TGGCACACTGCTCTTAAGAACTATGAWGATCTGAGATTTTTTTGTGTATGTTTTTGACTCTTTTGAGTGGTA  
ATCATATGTGTCTTTATAGATGTACATACCTCCTTGACAAATGGAGGGGAATTCATTTTCATCACTGGGAGT  
GTCCTTAGTGTATAAAAACCATGCTGGTATATGGCTTCAAGTTGTAAAAATGAAAGTGACTTTAAAGAAAAT  
AGGGGATGGTCCAGGATCTCCACTGATAAGACTGTTTTTAAGTAACTTAAGGACCTTTGGGTCTACAAGTAT  
ATGTGAAAAAATGAGACTTACTGGGTGAGGAAATTCATTGTTTAAAGATGGTCGTGTGTGTGTGTGTGTGT  
GTGTGTGTTGTGTTGTGTTTTGTTTTTAAGGGAGGGAATTTATTATTTACCGTTGCTTGAAATTACTGKGTA  
AATATATGTYTGATAATGATTTGCTYTTTGVCMACTAAAATTAGGVCTGTATAAGTWCTARATGCMTCCCTG  
GGKGTGATYTTCCMAGATATTGATGATAMCCCTTAAATTGTAACCYGCCTTTTTCCCTTTGCTYTCMATTA  
AAGTCTATTCMAAAG

17191.1&89.1

GGGGGTAGGCTCTTTATTAGACGGTTATTGCTGTACTACAGGGTCAGAGTGCAGTGTAAAGCAGTGTGAGAG  
GCCCCGCTTCAGCCCAAGAATGTGGATTTCTCTCCCTATTGATCACAGTGGGTGGGTTTCTTCAGAAAAG  
CCCCAGAGGCAGGGACCAGTGAGCTCCAAGGTTAGAAGTGGAAGTGGAAAGGCTTCAGTCACATGCTGCTT  
CCACGCTTCCAGGCTGGGCAGCAAGGAGGAGATGCCCATGACGTGCCAGGTCTCCCCATCTGACACCAGT  
GAAGTCTGGTAGGACAGCAGCCGCACGCCTGCCTCTGCCAGGAGGCCAATCATGGTAGGCAGCATTGCAG  
GGTCAGAGGTCTGAGTCCGGAATAGGAGCAGGGGCAGGTCCCTGCGGAGAGGCACTTCTGGCCTGAAGA  
CAGCTCCATTGAGCCCCTGCAGTACAGGYGTAGTGCTTGGACCAAGCCCACAGCCTGGTAAGGGGGCGCC  
TGCCAGGGCCACGGCCAGGAGGCA

**"REPLACEMENT SHEETS"**

**17192.1&2**

TAATTTCTTAGTCGTTTGAATCCTTAAGCATGCAAAAGCTTTGAACAGAAGGGTTACAAAAGGAACCAGGG  
TTGTCTTATGGCATCCAGTTAAGCCAGAGCTGGGAATGCCTCTGGGTCATCCACATCAGGAGCAGAAGCAC  
TTGACTTGTCGGTCCTGCTGCCACGGTTTGGGCGCCACCACGCCACGTCCACCTCGTCCTCCCCTGCC  
GCCACGTCTGGGCGGCCAAGGTCTCCAAAATTGATCTCCAGCTGAGACGTTATATCATTTGCTGGCTTCC  
GGAAATGATGGTCCATAACCGAATCTTCAGCATGAGCCTCTTCACTCTTTGATTTATGAAGAACAAATCCCTT  
CTTCCACTGCCCATCAGCACCTTCATTTGGTTTTCGGATATTAAATTCTACTTTTGCCCGGTCCTTATTTGA  
ATAGCCTTCCACTCATCCAAAGTCATCTCTTTTGACCCTCCTCTTTTACCTCTTCAACTTCATTCTCCTTATT  
TTCAGTGTCTGCCACTGGATGATGTTCTTCACCTTCAGGTGTTTCCTCAGTCACATTTGATTGATCCAAGTCA  
GTTAATTCGTCTTTGACAGTTCCCCAGTTGTGAGATCCGCTACCTCCACGTTTGTCTCGTGCTTCAGGCCA  
GATCTATCACTTCCACTATGCCTATCAAATTCACGTTTGCCACGAGAATCAAATCCATCTCCTCGGCCCAT  
CCACGTCCACGGCCCCCTCGACCTCTTCCAAGACCACCACGACCTCGAATAGGTCGGTCAATAATCGGTCT  
ATCAACTGAAAATTCGCCTCCTTCACCCTTTTCTTCAAGTGCGCTTTTCGAATCTTCGTTACGAGGTGGTCG  
CCTTTCTGGTCTTCTATCAATTATTTCCCTTCACCCTGAAGTTGTTGATCAGGTCTTCTTCCAACCTCGTGC

**17193**

AAGCGGATGGACCTGAGTCAGCCGAATCCTAGCCCCTTCCCTTGGGCCTGCTGTGGTGCTCGACATCAGT  
GACAGACGGAAGCAGCAGACCATCAAGGCTACGGGAGGCCCGGGGCGCTTGCGAAGATGAAGTTTGGCT  
GCCTCTCCTTCCGGCAGCCTTATGCTGGCTTTGTCTTAAATGGAATCAAGACTGTGGAGACGCGCTGGCGT  
CCTCTGCTGAGCAGCCAGCGGAAGTGTACCATCGCCGTCCACATTGCTCACAGGGACTGGGAAGGCGATG  
CCTGTGCGGAGCTGCTGGTGGAGAGACTCGGGATGACTCCTGCTCAGATTCAGGCCTTGCTCAGGAAAGG  
GGAAAAGTTTGGTGCAGGAGTGATAGCGGGACTCGTTGACATTGGGGAACTTTGCAATGCCCCGAAGAC  
TAACTCCCGATGAGGTTGTGGAAGTAGAAAATCAAGCTGCACTGACCAACCTGAAGCAGAAGTACCTGAC  
TGTGATTTCAAACCCAGGTGGTTACTGGAGCCCATACCTAGGAAAGGAGGCAAGGATGTATTCCAGGTAG  
ACATCCCAGAGCACCTGATCCCTTTGGGGCATGAAGTGTGACAAGTGTGGGCTCCTGAAAGGAATGTTCCR  
GAGAAACCAGCTAAATCATGGCACCTTCAATTTGCCATCGTGACGCAGACCTGTATAAATTAGGTTAAAGAT  
GAATTTCCACTGCTTTGGAGAGTCCCACCCACTAAGCACTGTGCATGTAAACAGGTTTCCTTTGCTCAGATGA  
AGGAAGTAGGGGGTGGGGCTTTCCTTGTGTGATGCCTCCTTAGGCACACAGGCAATGTCTCAAGTACTTTG  
ACCTTAGGGTAGAAGGCAAAGCTGCCAGTAAATGTCTCAGCATTGCTGCTAATTTTGGTCCTGCTAGTTTCT  
GGATTGTACAAATAAATGTGTTGTAGATGA

**16443.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCT  
GCCCATTTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGAC  
CTGGTTCTTGGTCATCTCCTCCCGGGATGGGGGCAGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTG  
GCTTTGGAGATGGTTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTACTCCTTGCC  
ATTCAACCAGTCCTGGTGCANGACGGTGAGGACGCTNACCACACGGTACGNGCTGGTGTACTGCTCCTCC  
CGCGGCTTTGTCTTGGCATTATGCACCTCCACGCCGTCCACGTACCAATTGAACCTTGACCTCAGGGTCTTC  
GTGGCTCACGTCCACCACCACGCATGTAACCTCAAANCTCGGNCGCCANACGC

**16443.2.edit**

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT  
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC  
AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA  
AGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCC  
CCGAGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACC  
TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA  
CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACACCTGCCGGGCGGCCGCTCGA

**16444.2.edit**

AGCGTGGTTNCGGCCGAGGTCCCAACCAAGGCTGCANCTGGATGCCATCAAAGTCTTCTGCAACATGGA  
GACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCAGAGAAGTGGTACATCAGCAAGAAC  
CCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCC  
AGGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGNCGCTCGA

**16445.1.edit**

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGACT  
GGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAAC  
ATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCAGAGAAGTGGTACATCAGCA  
AGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG  
CGGCCAGGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA



**16445.2.edit**

TCGAGCGGTGCGCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAAT  
CCATCGGNCATGCTCTCGCCGAACCAGACATGCCTCTTGNCCTTGGGGTTCTTGCTGATGTACCAGNTCTT  
CTGGGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCANTCTCCATGTTGCANAAGACTTTGATG  
GCATCCAGGTTGCAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGACAGAGTGGCACATCTT  
GAGGTCACGGCAGGTGCGGGCGGGGTTCTTGACCTCGGTGCGGACACGCT

**16446.1.edit**

TCGAGCGGCCGCGCCGGGCAGGTCCCTCCTCAGAGCGGTAGCTGTTCTTATTGCCCCGGCAGCCTCCATAGA  
TNAAGTTATTGCANGAGTTCCTCTCCACGTCAAAGTACCAGCGTGGGAAGGATGCACGGCAAGGCCAGT  
GACTGCGTTGGCGGTGCAGTATTCTTCATAGTTGAACATATCGCTGGAGTGGACTTCAGAATCCTGCCTTCT  
GGGAGCACTTGGGACAGAGGAATCCGCTGCATTCTGCTGGTGGACCTCGGCCGCGACACGCT

**16446.2.edit**

AGCGTGGTGC CGGCCGAGGTCCACCAGCAGGAATGCAGCGGATTCCTCTGTCCCAAGTGCTCCCAGAAG  
GCAGGATTCTGAAGACCACTCCAGCGATATGTTCAACTATGAAGAATACTGCACCGCCAACGCAGTCACTG  
GGCCTTGCCGTGCATCCTTCCCACGCTGGTACTTTGACGTGGAGAGGAACTCCTGCAATAACTTCATCTAT  
GGAGGCTGCCGGGGCAATAAGAACAGCTACCGCTCTGAGGAGGACCTGCCCGGGCGGCCGCTCGA

**16447.1.edit**

TCGAGCGGCCGCGCCGGGCAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAAT  
CCATCGGTGCTGCTCTCGCCGAACCAGACATGCCTCTTGTCCTTGGGGTTCTTGCTGATGTACCAGTTCTT  
CTGGGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATG  
GCATCCAGGTTGCAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAATGGCACATCTT  
GAGGTCACGGCANGTGC GGCGGGGTTCTTGACCTCGGCCGCGACACGCT

**16447.2.edit**

AGCGTGGTCGCGGCCGAGGTCAAGAAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGG  
CTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCA  
ACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAAGTGGTACATCAG  
CAAGAACCCCAAGGACAAGAGGCATGTCTGGCTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTAT  
GGCGGCCAGGGCTCCGACCCTGCCGATGTGGACCTGCCCCGGCGGCCGCTCGA

**16449.1.edit**

AGCGTGGTCGCGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGNTCCAGGAACCCTGAACTGTAAGG  
GTTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGNAATGGGGCCCATGAN  
ATGGTTGNCTGAGAGAGAGCTTCTTGTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGT  
GGCCGTTGNGGGCGGTGNGGTCCGCCTAAAACCATGTTCTTCAAAGATCATTTGTTGCCAACACTGGGTT  
GCTGACCANAAGTGCCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGT  
CTTTTGAAGTGTGGAAGGAACATCCAAGATCTCTGNTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTT  
GGGGAAGCTCGCTGTCTTTTCTTCCAATCANGGGCTCGCTCTTCTGAATATTCTTCAGGGCAATGACATA  
AATTGTATATTCGGTTCCTCGGTTCCAGGCCAG

**16450.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCA  
GGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCG  
CCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCAATTGCC  
TGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACC  
CTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTC  
ACCCACCCTGGGTATGACACTGGAAATGGTATTCAGCTTCTTGGCACTTCTGGTCAGCAACCCAGTGTGG  
GCAACAAATGATCTTTGANGAACATGGNTTTAGGCGGACCACACCGGCCACAACGGGCACCCCCATAAGG  
CATAGGCCAAGAACATACCCGNCGAATGTAGGACAAGAAGCTCTNTCTCANACAANCATCTCATGGGCCCC  
ATTCCANGACACTTCTGAGTACATCANTTCATGGCATCCTGGTGGCACTGATAAAAACCTTACAGTTA

**16450.2.edit**

AGCGTGGTCGCGGGCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGG  
GTTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAG  
ATGGTTGTCTGAGAGAGAGCTTCTTGTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGT  
GGCCGTTGTGGGCGGTGTGGTCCGCCTAAAACCATGTTCTTCAAAGATCATTTGTTGCCAACACTGGGTT  
GCTGACCAGAAGTGCCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGT  
CTTTTGAAGTGTGGAAGGAACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTT  
GGGGAAGCTCGTCTGTCTTTTCTTCCAATCANGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACAT  
AAATTGTATATTCGGNTCCCGGTTNCAGCCAATAATAAACCTCTGTGACACCANGGCGGGGCCGAAGG  
ANCACT

**16451.1.edit**

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTACCACCTACAACATCATAGTGGAGGCACTGAAAGACC  
AGCAGAGGCATAAGGTTCTGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACC  
TACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGT  
CTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTAGATGTGATTCATCTA  
GATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACC  
TGCCCCGGGCGGCCGCTCGA

**16451.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACAC  
CATTGTGATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACA  
GTTTAAAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA  
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGNTGACAGAGTTGCCACGGTAACAACCTCTTCCCGA  
ACCTTATGCCTCTGCTGGTCTTTAGTGCCCTCACTATGATGTTGTAGGTGGTACCTCTGGTGAGGACCTC  
GGCCGCGACCACGCT

**16452.1.edit**

AGCGTGGCCGCGGCCGAGGTCCATTGGCTGGAACGGCATCAACTTGAAGCCAGTGATCGTCTCAGCCTT  
GGTTCTCCAGCTAATGGTGATGGNGGTCTCAGTAGCATCTGTCACACGAGCCCTTCTTGGTGGGCTGACAT  
TCTCCAGAGTGGTGACAACACCCTGAGCTGGTCTGCTTGTCAAAGTGTCTTAAGAGCATAGACACTCACT  
TCATATTTGGCGNCCACCATAAGTCCTGATACAACCACGGAATGACCTGTCAGGAAC

**16452.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCTCAGACCGGGTTCTGAGTACACAGTCAGTGTGGTTGCCTTGCACGA  
TGATATGGAGAGCCAGCCCCTGATTGGAACCCAGTCCACAGCTATTCCTGCACCAACTGACCTGAAGTTCA  
CTCAGGTCACACCCACAAGCCTGAGCGCCAGTGGACACCACCCAATGTTGAGCTCACTGGATATCGAGT  
GCGGGTGACCCCAAGGAGAAGACCGGACCAATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGTG  
GTTGTATCAGGACTTATGGCGGCCACCAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTTGACAAGC  
AGACCAGCTCAGGGTGTGTCACCACTCTGGAGAATGTCAGCCACCAAGAAGGGCTCGTGTGACAGATG  
CTACTGAGACCACCATCACCATTAGCTGGAGAACCAAGACTGAGACGATCACTGGCTTCCAAGTTGATGCC  
GTTCCAGCCAATGGACCTCGGCCGCGACCACGCTT

**16453.1.edit**

AGCGTGGTCGCGGCCGAGGTCTGGCCGAAGTGTACAGGGAAGATGTACATGTTATAGNTCTTCT  
CGAAGTCCCGGGCCAGCAGCTCCACGGGGTGGTCTCCTGCCTCCAGGCGCTTCTCATTCTCATGGATCTT  
CTTCACCCGCAGCTTCTGCTTCTCAGTCAGAAGGTTGTTGTCTCATCCCTCTCATACAGGGTGACCAGGA  
CGTTCTTGAGCCAGTCCCGCATGCGCAGGGGGAATTCGGTCAGCTCAGAGTCCAGGCAAGGGGGGATGT  
ATTTGCAAGGCCCGATGTAGTCCAAGTGGAGCTTGTGGCCCTTCTTGGTGCCCTCCAAGGTGCACTTTGTG  
GCAAAGAAGTGGCAGGAAGAGTCAAGGTCTTGTTGTCATTGCTGCACACCTTCTCAAAGTGGCAATGGG  
GGCTGGGCAGACCTGCCCGGGCGGCCGCTCGA

**16453.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTGCCCAGCCCCCATTGGCGAGTTTGAGAAGGNGTGCAGCAATGACA  
ACAAGACCTTCGACTCTTCTGCCACTTCTTTGCCACAAAGTGCACCCTGGAGGGCACCAAGAAGGGCCAC  
AAGCTCCACCTGGACTACATCGGGCCTTGAAATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATT  
CCCCCTGCGCATGCGGGACTGGCTCAAGAACGTCTGGTCACCCTGTATGAGAGGGATGAGGACAACAAC  
CTTCTGACTGAGAAGCANAAGCTGCGGGTGAAGAAATCCATGAGAATGANAAGCGCCTGNAGGCANGAG  
ACCACCCCGTGGAGCTGCTGGCCCCGGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGG  
CAGTTCGGCCAGACCTCGGCCGCGACCACGCT

**16454.1.edit**

AGCGTGGNTGCGGACGACGCCCCACAAAGCCATTGTATGTAGTTTTANTTCAGCTGCAAANAATACCNCCAG  
CATCCACCTTACTAACCAGCATATGCAGACA

**16454.2.edit**

TCGAGCGGTCGCCCCGGGCAGGTCTGGGCGGATAGCACCGGGCATATTTTGAATGGATGAGGTCTGGCA  
CCCTGAGCAGCCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGT  
TCTGAGTCTGTGGGATAGCTGCCATGAAGNAACCTGAAGGAGGCGCTGGCTGGTANGGGTTGATTACAGG  
GCTGGGAACAGCTCGTACACTTGCCATTCTCTGCATATACTGGNTAGTGAGGCGAGCCTGGCGCTCTTCTT  
TGCGCTGAGCTAAAGCTACATACAATGGCTTTGNGGACCTCGGCCGCGACCACGCTT

**16455.1.edit**

TCGAGCGGCCGCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACAC  
CATTGTCATGACACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACA  
GTTTAAAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA  
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAAGTTGCCACGGTAACAACCTCTTCCCG  
AACCTTATGCCTCTGCTGGTCTTTCAAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACC  
TCGGCCGCGACCAAGCT

**16455.2.edit**

AGCGTGGTTTTCGGCCGAGGTCTCACCANAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGAC  
CAGCAGAGGCATAAGGTTTCGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAAC  
CTACGGATGACTCGTGCTTTGACCCCTACACAGNTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATG  
TCTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGTCATTTGAGATGTGATTCATCT  
ANATGGTGTGATGACAATGGTGNGAACTACAAGATTGGAGAGAAGTGGNACCGTCAGGGGANAAAATGGA  
CCTGCCCGGGCGGCNCGCTCGA

**16456.1.edit**

AGCGTGGTCGCGGCCGAGGTCTGGCTTNCTGCTCANGTGATTATCCTGAACCATCCAGGCCAAATAAGCG  
CCGGCTATGCCCTGNATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAG  
ATTGATC

**16456.2.edit**

TCGAGCGGCCGCCGGGCAGGTCCAATTGAAACAAACAGTTCTGAGACCGTTCTTCCACCACTGATTAAGA  
GTGGGGNNGCGGGTATTAGGGATAATATTCATTTAGCCTTCTGAGCTTTCTGGGCAGACTTGGTGACCTTG  
CCAGCTCCAGCAGCCTTCTGGTCCACTGCTTTGATGACACCCACCGCAACTGTCTGTCTCATATCACGAAC  
AGCAAAGCGACCCAAAGGTGGATAGTCTGAGAAGCTCTCAACACACATGGGCTTGCCAGGAACCATATCAA  
CAATGGGCAGCATCACCAGACTTCAAGAATTTAAGGGCCATCTTCCAGCTTTTTACCAGAACGGCGATCAAT  
CTTTTCCTTCAGCTCAGCAAACCTTGCATGCAATGTGAGCCG

**16459.1.edit**

TCGAGCGGCCGCCCGGGCAGGTCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAA  
TTGCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTT  
GTGGNTACTGACCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGC  
GCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAAGGGAGCTCACT  
CAGNGGGGTTTGATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCATGCGTGGCACCATTTCCTGTAAC  
ACCCATGGGANGNCATGCCTGATCTGGACTTCTACAGAGATCCTGAAGAGATTGAAAAAGAAGAACAGGCT  
GNTTGCTGANAAAGCAAGTGACCAAGGANGAAATTTCANGGGTGAAANGGACTGCTCCCGCTCCTGAATTC  
ACTGCTACTCAACCTGANGNTGCAGACTGGTCTTGAAGNGNACANGGGCCCTCTGGGCCTATTTAAGCA  
NCTTCGGTCGCGAACACGNT

**16459.2.edit**

AGCGTGNGTCGCGGCCGAGGTGCTGAATAGGCACAGAGGGCACCTGTACACCTTCAGACCAGTCTGCAAC  
CTCAGGCTGAGTAGCAGTGAAGTCAAGAGCGGGAGCAGTCCATTACCCTGAAATTCCTCCTTGGNCACT  
GCCTTCTCAGCAGCAGCCTGCTCTTCTTTTCAATCTCTTCAGGATCTCTGTAGAAGTACAGATCAGGCATG  
ACCTCCCATGGGTGTTACGCGGAAATGGTGCCACGCATGCGCAGAACTTCCCGAGCCAGCATCCACCACA  
TCAAACCCACTGAGTGAGCTCCCTTGTTGTTGCATGGGATGGGCAATGTCCACATAGCGCAGAGGAGAATC  
TGTGTTACACAGCGCAATGGTAGGTAGGTTAACATAAGATGCCTCCGCGAGAAGCTGGTGGTCAGCCCTG  
GGGTCAAGTAACCACAAGAAGCCGTGGCTCCCGGAAGGCTGCCTGGATCTGGTTAGTGAAGGNTCCAGGA  
GTGAAGCGGCCAACAAATTGGAGTGGCTTCAGTGGCAAGCAGCAAACCTTCAGCACAAGCCCTCTGGACCTG  
CCCGGCGGCCGCTCGA

**16460.1.edit**

TCGAGCGGCCGCCCGGGCAGGTCCATTTTCTCCCTGACGGNCCCACTTCTCTCCAATCTTGTAGTTCACAC  
CATTGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACA  
GTTTAAAGCCTGATTACAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA  
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCNTCCCCG  
AACCTTATGCCTCTGCTGGGCTTTCAGNGCCTCCACTATGATGNTGTAGGGGGGCACCTCTGGNGANGAC  
CTCGGCCGCGACCAAGCT

**16460.2.edit**

AGCGTGGTCGCGGCCGAGGTCCCTACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACC  
AGCAGAGGCATAAGGCTCGGGAAGAGGTTGTTACCGTGGGCACTCTGTCAACGAAGGCTTGAACCAACC  
TACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGT  
CTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTANGCTTTGGAAGTGGGTCATTTAGATGTGATTCATCT  
AGATGGTGCCATGACAATGGNGNGAACTACAAGATTGGAGAGAAGTGGNACCGNCAGGGAGAAAATGGAC  
CTGCCCCGGCGGCCGCTCGA

**16461.1.edit**

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCC  
ATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTG  
GGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCA  
TCCAGGNTGCAACCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGCCAGAGTGGCACATCTTGAG  
GTCACGGCAGGTGCGGNCGGGGNTTTTGCGGCTGCCCTCTGGNCTTCGGNTGTNCTCNATCTGCTGGC  
TCA

**16461.2.edit**

TCGAGCGGCCGCCCGGGCAGGTCTCGCGGTCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCT  
CCTGGACCTCCTGGCCCCCCTGGTCCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTC  
AAGAGAAGGCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTTCGTGACCGTGACCT  
CGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGNCG  
CAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGG  
ATTGACCCCAACCAAGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGC  
GTGTACCCCACTCAGCCAGTGTGGCCCAAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAAGC  
ATGTCTGGTTCGGCGAGAACATGACCGATGGATTCCAGTTCGAGTATGGCGGGCAGGGCTCCGACCCTGC  
CGATGGGGACCTTGGCCGCGAACACGCT

**16463.1.edit**

AGCGTGGNNGCGGCCGAGGTATAAATATCCAGNCCATATCCTCCCTCCACACGCTGANAGATGAAGCTGT  
NCAAAGATCTCAGGGTGGANAAAACCAT

**16463.2.edit**

TCGAGCGGCCGCCCGGGCAGGTCCTTCAGACTTGGACTGTGTCACACTGCCAGGCTTCAGGGCTCCAAC  
TTGCAGACGGCCTGTTGTGGGACAGTCTCTGTAATCGCGAAAGCAACCATGGAAGACCTGGGGGAAAACA  
CCATGGTTTTATCCACCCTGAGATCTTTGAACAACTTCATCTCTCAGCGTGCGGAGGGAGGCTCTGGACTG  
GATATTTCTACCTCGGCCGCGACCAACGCT

**16464.1.edit**

CGAGCGGGCGACCGGGCAGGTNCAGACTCCAATCCANANAACCATCAAGCCAGATGTCAGAAGCTACACC  
ATCACAGGTTTACAACCAGGCACTGACTACAAGANCTACCTGCACACCTTGAATGACAATGCTCGGAGCTC  
CCCTGTGGTCATCGACGCCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCA  
ATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGTACATCATCNAGTATGANAAGCCTG  
GGCCTCCTCCCAGAGAAGNGGTCCCTCGGCCCGGCCCTGNTGTCCCANAGGNTACTATTACTGNGCCNGC  
AACCGGCAACCGATATCNATTTTGNCATTGGCCTTCAACAATAATTA

**16464.2.edit**

AGCGTGGTTCGCGGCCGANGTCCTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGG  
GTTCTTCATCAGNGCCAACAGGATGACATGAAATGATGTAAGTGTCTGGAATGGGGCCCATGAG  
ATGGTTGTCTGAGAGAGAGCTTCTTGNCCTGTCTTTTTCCTTCCAATCAGGGGCTCGCTCTTCTGATTATTC  
TTCAGGGCAATGACATAAATTGTATATTCGGGTCCCGGNTCCAGGCCAGTAATAGTANCCTCTGTGACACC  
AGGGCGGNGCCGAGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTAACCGGTA  
ATCCTGGCACGTGGCGGCTGCCATGATACCAGCAAGGAATTGGGGTGTGGTGGCCAGGAAACGCAGGTT  
GGATGGNGCATCAATGGCAGTGGAGGCCGTGATGACCACAGGGGGAGCTCCGACATTGTCATTCAAGGT  
G

**16465.1.edit**

AGCGTGGNCGCGGCCGAGGTGCAGCGCGGGCTGTGCCACCTTCTGCTCTCTGCCCAACGATAAGGAGGG  
TNCTGCCCCCAGGAGAACATTAACNTNTCCCGAGCTCGGCCTCTGCCGG

**16465.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTTTTTTTTGCTGAAAGTGGNTACTTTATTGGNTGGGAAAGGGAGAAGCT  
GTGGTCAGCCCAAGAGGGAATACAGAGNCCCGAAAAAGGGGAGGGCAGGTGGGCTGGAACCAGACGCAG  
GGCCAGGCAGAACTTTCTCTCCTCACTGCTCAGCCTGGTGGTGGCTGGAGCTCANAAATTGGGAGTGAC  
ACAGGACACCTTCCCACAGCCATTGCGGCGGCATTTTCATCTGGCCAGGACACTGGCTGTCCACCTGGCAC  
TGGTCCCGACAGAAGCCCCGAGCTGGGGAAAGTTAATGTTACCTGGGGGCAGGAACCCTCCTTATCATTG  
NGCAGAGAGCAGAAGGTGGCACAGCCCCGCGCTGCACCTCGGCCGCGACCACGCT

**16466.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGT  
TGATTTCTTTCATTGGTCCGGNCTTCTCCTTGGGGGNCACCCGCACTCGATATCCAGTGAGCTGAACATTG  
GGTGGCGTCCACTGGGCGCTCAGGCT

**16467.2.edit**

TCGAGCGGTTGCCCCGGGCAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCC  
AGGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCAGAGAAGCGGTCCCTCGGCCCC  
GCCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGNC  
CTGAAGAATAATCANNAANAGCGANCCCCTGATTGGAAGGA





06\_16471.edit

AGCGTGGTCGCGGCCGAGGTCTGCTGCTTCAGCGAAGGGTTTCTGGCATAACCAATGATAAGGCTGCCAA  
AGACTGTTCCAATACCAGCACCAGAACCAGCCACTCCTACTGTTGCAGCACCTGCACCAATAAATTTGGCA  
GCAGTATCAATGTCTCTGCTGATTGCACTGGTCTGAACTCCCTTTGGATTAGCTGAGACACACCATTCTGG  
GCCCTGATTTTCTAAGATAGAACTCCAACCTCTTTGCCCTCTAGCACATAGCCATCTGCTCGGTCACTGT  
CCCGGCCCTTGAAGCGATGCACGCAAGAAGCTTGCCCTGCTGGAAGTCTCCTCCAGGAGACTGCTGATTT  
TGGCATTCTTTTTCTTTTCATCATATTTCTTCTGAATTTTTTTAGATCGTTTTTTGTTTAAATCTCTTCTTCT  
CAGGAGTCAGCTTGGCCCCCGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCC  
CTGAGGTTGGACGTGGGGAATTTCTCCTGGGGCTCAGAGTGGTGTACTCGTAAAACAAGGATCATCGATG  
GTGNCTACAATGCATCTAATAACGAGCTGGGTGCGACCCAAAGAACCTGGNGAANAATGGATCGNCTCAT  
CGACAGGACACCGTACCCGACAGGGGNACGANTCCCACTATGCGCTTGCCCTGGGCCGCAANAAAGGA  
AAACTGCCCCGGCGGCCNTCGAAAGCCCAATTNTGAAAAAATCCATCACACTGGGNGGCCNGTCGAGCA  
TGCATNTANAGGGGCCCATTCCTCCCTNANN

07\_16472.edit

TCGAGCGGCCGCCCCGGGCAGGTCCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACAT  
GGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAAGAAGTGGTACATCAGCAAG  
AACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCG  
GCCAGGGCTCCGACCCTGCCGATGTGGACCTCGGCCGCGACCACGCT

08\_16472.edit

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTGGAGCCCTGGCCGCCATACTCGAACTGGAATCC  
ATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTCTTGCTGATGTACCAGTTCTTCTG  
GGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCA  
TCCAGGTTGCAGCCTTGTTGGGGACCTGCCCGGGCGGCCGCTCGA

09\_16473.edit

TCGAGCGGCCGCCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCA  
GGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCG  
CCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCC  
TGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACC  
CTTCCACACCCCAATCTTCATGGACCAGAGATCTTGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTC  
ACCCACCCTGGGTATGACACTGGAAATGGTATTCAGCTTCTGCTGCACTTCTGGTCAGCAACCCAGTGTGG  
GCAACAAATGATCTTTGAGGAACATGGNTTTAGGCGGACCACACCGCCCAACGCGCCACCCCCATAAGG  
CATAGGCCAAGACCATAACCGCCGAATGTAGGACAAGAAGCTNTNTNNTCANACACCATNTNATGGGCCCCA  
TTCCAGGACACTTCTGAGTACATCATTTATGNCATCTGTGGCACTTGATGAAAACCTTACAGTTCAGGGTT  
CTGGAACTTTTACCAGGCCTNTTACAGGACTNGGCCGGACNCCTTAAGCCNATTNCACCCTGGGGCGTTCT  
ANGGTCCCACTCGNNCACTGGNGAAAATGGCTACTGTN

11\_16474.edit

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCCAGGCAGAGTCTCTGCGTTACAAA  
CTCCTAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCC  
AAAGGCTGCGAGGTTGTGGTGTCTGNAACTCCNAGGACANGAGGGCTAAATTCCATGAAGTTTGTGGAT  
GGCCTGATGATCCACAATCGGAGACCCTGTAACTACTACCGTCTNACCNCCTGCTGTNCNCCCCCNTTTC  
TGCTNAANACATNGGGNTNNTNCTTGNCNTCCTTGCGTNGAANATNNAATNGCCTNCCCNTTCNTANCNC  
TACTNGNTCCANANTTGGCCTTTAAANAATCCNCCTTGCTTNNNCACTGTTCANNTNTTNTNNTCGTAAACC  
CTATNANTTNATTANATNNTNNNNNCTCACCCCTCCTCATTNANCCNATANGCTNNNAANTCCTTNAN  
NCCTCCCNCCNNTNCNCTCCTACTNANTNCTTCTNNCCCATTACNNAGCTCTTTCNTTTAANATAATGNNG  
CCNNGCTCTNCATNTCTACNATNTGNNAATNCCCCNCCCCNANCGNNTTTTTGACCTNNNAACCTCCT  
TTCCTCTTCCCTNCNNAATTCNNANTTCCNCNTTCCNNCNTTTCGGNTNNTCCCATNCTTTCANNNCTT  
CANTCTANCNCNCTNCAACTTATTTTCTNTCATCCCTTNTTCTTTACANNCCCCCTNNTCTACTCNCNNTT  
NCATTANATTTGAACTNCCACNNCTANTTNCCTCNCCTCTACNNTTTTATTTTNCGNTCNCCTCTACNTAATAN  
TTAATNANTTNTCN

12\_16474.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGC  
AGGCGGCTCTGGCTTCCCACCCTTCTGTTCTGAGATGGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCA  
CAATGCTCACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCCAGGGCAGCATGAT  
CTTCACCTTGATGCCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAAGCAGTGTCAACGTAGTAAGTT  
AACAGGGTCTCCGCTGTGGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCTCGGAGTT  
TCCCAGACACCACAACCTCGCAGCCTTTGGCCCCACTCTCCATGATGAACCGCAGCACACCATAGCAGGC  
CCTCCGCACAAGCAAGCCCTCCTAAGAATTTGTAACGCANANACTCTGCTGGCAATGGCACACAAACCTCT  
AGTGGACCTCGGNCGCGACACGC

13\_16475.edit

TCGAGCGGCCGCCCCGGGCAGGTCTGGTCCAGGATAGCCTGCGAGTCCTCCTACTGCTACTCCAGACTTGA  
CATCATATGAATCATACTGGGGAGAATAGTTCTGAGGACCAGTAGGGCATGATTCACAGATTCCAGGGGGG  
CCAGGAGAACCAGGGGACCCTGGTTGTCCTGGAATACCAGGGTCACCATTTCTCCCAGGAATACCAGGAG  
GGCCTGGATCTCCCTTGGGGCCTTGAGGTCTTGACCATTAGGAGGGCGAGTAGGAGCAGTTGGAGGCTG  
TGGGCAAACTGCACAACATTCTCCAAATGGAATTTCTGGGTTGGGGCAGTCTAATTCTTGATCCGTCACATA  
TTATGTCATCGCAGAGAACGGATCCTGAGTCACAGACACATATTTGGCATGGTTCTGGCTTCCAGACATCTC  
TATCCGNCATAGGACTGACCAAGATGGGAACATCCTCCTTCAACAAGCTTNTGTTGTGCCAAAAATAATAG  
TGGGATGAAGCAGACCGAGAAGTANCCAGCTCCCCTTTTGCACAAAGCNTCATCATGTCTAAATATCAGA  
CATGAGACTTCTTTGGGCAAAAAAGGAGAAAAAGAAAAAGCAGTTCAAAGTANCCNCCATCAAGTTGGTTCC  
TTGCCNTTCAGCACCCGGGCCCGTTATAAAACACCTNNGGGCCGGACCCCTT

*Fig. 15GG*

**14\_16475.edit**

AGCGTGGTCGCGGCCGAGGTGTTTTATGACGGGCCCCGGTGCTGAAGGGCAGGGAACAACCTTGATGGTGC  
TACTTTGAACTGCTTTTCTTTTCTCCTTTTGCACAAAGAGTCTCATGTCTGATATTTAGACATGATGAGCTTT  
GTGCAAAAGGGGAGCTGGCTACTTCTCGCTCTGCTTCATCCCACTATTATTTGGCACAACAGGAAGCTGTT  
GAAGGAGGATGTTCCCATCTTGGTCAGTCCTATGCGGATAGAGATGTCTGGAAGCCAGAACCATGCCAAAT  
ATGTGTCTGTGACTCAGGATCCGTTCTCTGCGATGACATAATATGTGACGATCAAGAATTAGACTGCCCCAA  
CCCAGAAATTCCATTTGGAGAATGTTGTGCAGTTTGCCACAGCCTCCAACCTGCTCCTACTCGCCCTCCTAA  
TGGTCAAGGACCTCAAGGCCCAAGGGAGATCCAGGCCCTCCTGGTATTCCTGGGAGAAATGGTGACCCT  
GGTATTCAGGACAACCAGGGTCCCCTGGTTCTCCTGGCCCCCTGGAATCNGGNGAATCATGCCCTACT  
GGTCTCAAACCTATTCTCCANATGATTCATATGATGTCAAGTCTGGGATAGCNAGTANGGANGGACTCGC  
AGGCTATTCTGGACCANACCTGCCGGGGGGGCGTTGAAAGCCCCGAATCTGCANANNTNCNTTCACACTG  
GCGGCCGTCGAGCTGCTTTAAAAGGGCCATTCCNCCTTTAGNGNGGGGGANTACAATTACTNGGCGGCGT  
TTANANCGCGNGNCTGGGAAAT

**15\_16476.edit**

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCC  
ATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTG  
GGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCA  
TCCAGGTTGCAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAG  
GTCACGGCAGGTGCGGGCGGGGTTCTTGCGGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCT  
CAGGCTCTTGAGGGTGGTGTCCACCTCGAGGTACGGTCACGAACCACATTGGCATCATCAGCCCGGTAG  
TAGCGGCCACCATCGTGAGCCTTCTTGTANGTGGCTGGGGCAGGAAGTGAAGTCGAAACCAGCGCTGGG  
AGGACCAGGGGGACCAANAGGTCCAGGAAGGGCCCCGGGGGGGACCAACAGGACCAGCATCACCAAGTG  
CGACCCGCGAGAACCTGCCCGGCCGNCCGCTCGAA

**16\_16476.edit**

TCGAGCGNNCGCCCGGGCAGGTCTCGCGGTGCGACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCT  
CCTGGACCTCCTGGTCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTC  
AAGAGAAAGGCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCT  
CGAGGTGGACACCACCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGCCG  
CAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGG  
ATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG  
CGTGTACCCCACTCAGCCCAGTGTGGCCGAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGG  
CATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCCACCCTG  
CCGATGTGGACCTCCGGCCGCGACCACCTT

17\_16477.edit

TNGAGCGGCCGCCGGGCAGGNTGNNAACGCTGGTCCTGCTGGTCCTCCTGGCAAGGCTGGTGAAGATG  
GTCACCTTGGAAAACCCGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCC  
TGGAACCTCCTGGACTTCCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAG  
CCCGGTGCTCCTGGTGTGAAGGGTGAACCTGGTGCCCTGGTGAAAATGGAACCTCAGGTCAAACAGGAG  
CCCGTGCGCTTCCTGGTGAGAGAGGACCGTGTTGGTGCCCTGGCCCANACCTCGGCCGCGACCACGCT  
AAGCCCGAATTTCCAGCACACTGGNGGCCGTTACTANTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATC  
ATGGTCATAGCTGTTTCCTGNGTGAAATTGTTATCCGCTCACAATTTACACANCATACGAAGCCGGAAAGC  
ATAAAGTGTAAGCCTTGGGGTGCTAATGAGTGAGCTAACTCNCATTAAATTGCGTTGCGCTCACTGCCCG  
CTTTTCCANNNGGAAACCNTGGCNTNGCCNGCTTGCTNTAANTGAAATCCGCCNACCCCGGGGAAAAG  
NCGGTTTGCGTATTGGGGCNCCTTTTCCCTTTCCTCGGNTTACTTGANTTANTGGGCTTTGGNCGNTTCG  
GGTTGNGGCGANCNGGTTCAACNTCACNCAAAGGNGGNAANACGGTTTTCCANAATCCGGGGGNTANC  
CCAANGNAAAACATNNGNCNAANGGCT

18\_16477.edit

AGCGTGGTTNGCGGCCGAGGTCTGGGCCAGGGGCACCAACACGTCCTCTCTCACCAGGAAGCCCACGGG  
CTCCTGTTTGACCTGGAGTTCCATTTTACCAGGGGGCACCAGGTTACCCTTCACACCAGGAGCACCAGGGC  
TGTCCTTCAATCCATNCAGACCATTGTGNCCCCTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCAGG  
GAAACCACCGAGCACCCTGTGGTCCAACAACCTCTCTCACCAGGTCGTCCGGGTTTTCCAGGGTGACC  
ATCTTCACCAGCCTTGCCAGGAGGACCAGCAGGACCAGCGTTACCAACCTGCCCGGGCGGCCGCTCGA

21\_16479.edit

TCGAGCGGCCGCCGGGCAGGTCCATTTTCTCCCTGACGGTCCCCTCTCTCCAATCTTGTAGTTCACAC  
CATTGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCAAAGCCTAAGCACTGGCACAACA  
GTTTAAAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA  
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGA  
ACCTTATGCCTCTGCTGGTCTTTCAGTGCCCTCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTC  
GGCCGCGACCACGCT

22\_16479.edit

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGAGGGCACTGAAAGACC  
AGCAGAGGCATAAGGTTGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACC  
TACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGT  
CTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTCAAGATGTGATTCATCT  
AGATGGTGCCATGACAATGGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGAC  
CTGCCCGGGGCCGGCCGCTCGA

**24\_16480.edit**

TCGAGCGNNCGCCCGGGCAGGTCCAGTAGTGCCTTCGGGACTGGGTTCACCCCCAGGTCTGCGGCAGTT  
GTCACAGCGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGC  
CACTGTTCTCCTACGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCT  
CCTTTTCCGTTCCCAAGACATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGGAAAGTTTGTGAAACTG  
TGCCACTGACCTTTACTTCTCTCTCTACTGGAGCTTTCGTACCTTCCACTTCTGCTGTTGGTAAAATGGT  
GGATCTTCTATCAATTTTCATTGACAGTACCCACTTCTCCCAAACATCCAGGGAAATAGTGATTTTCAGAGCGA  
TTAGGAGAACCAAATTATGGGGCAGAAATAAGGGGCTTTTCCACAGGTTTTCCTTTGGAGGAAGATTTTCAGT  
GGTGACTTTAAAAGAATACTCAACAGTGTCTTCATCCCATAGCAAAAAGAAGAAACNGTAAATGATGGAANG  
CTTCTGGAGATGCCNNCATTTAAGGGACNCCCAGAACTTCACCATCTACAGGACCTACTTCAGTTTACANNA  
AGNCACATANTCTGACTCANAAAGGACCCAAGTAGCNCCATGGNCAGCACTTTNAGCCTTTCCCTGGGGA  
AAANNTTACNTTCTTAAANCCTNGGCCNNGACCCCTTAAGNCCAAATTNTGGAAAANTTCCNTNCNNCTGG  
GGGGCNGTTCNACATGCNTTTNAAGGGCCCAATTNCCCCNT

**25\_16481.edit**

TCGAGCGGCCCGCCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCT  
GCCCATTTGCTCTCCCACTCCACGGCGATGTGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGAC  
CTGGTTCTTGGTCATCTCCTCCCGGGATGGGGGCAGGGTGTACACCTGTGGTTCTCGGGGCTGCCCTTTG  
GCTTTGGAGATGGTTTTCTCGATGGGGGCTGGGAGGGCTTTGTTGGAGACCTTGCACTTGTACTCCTTGCC  
ATTCAGCCAGTCCTGGTGCAGGACGGTGAGGACGCTGACCACACGGTACGTGCTGTTGTACTGCTCCTCC  
CGCGGCTTTGTCTTGGCATTATGCACCTCCACGCCGTCCACGTACCAAGTTGAAGTTGACCTCAGGGTCTTC  
GTGGCTCACGTCCACCACCACGCATGTAACCTCAGACCTCGGCCGCGACACGCT

**26\_16481.edit**

AGCGTGGTTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT  
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC  
AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA  
AGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAAGC  
CCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGAC  
CTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA  
CAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACACCTGCCCGGGCGGGCGCTCGA

**27\_16482.edit**

TCGAGCGGCCCGCCCGGGCAGGTTGAATGGCTCCTCGCTGACCACCCCGGTGCTGGTGGTGGGTACAGAG  
CTCCGATGGGTGAAACCATTGACATAGAGACTGTCCCTGTCCAGGGTGTAGGGGCCAGCTCAGTGATGC  
CGTGGGTGAGCTGGCTCAGCTTCCAGTACAGCCGCTCTCTGTCCAGTCCAGGGCTTTTGGGGTCAGGACG  
ATGGGTGCAGACAGCATCCACTCTGGTGGCTGCCCCATCCTTCTCAGGCCTGAGCAAGGTGAGTCTGCAA  
CCAGAGTACAGAGAGCTGACACTGGTGTCTTGAACAAGGGCATAAGCAGACCCTGAAGGACACCTCGGC  
CGCGACCACGCT

**28\_16482.edit**

AGCGTGGTCGCGGCCGAGGTGTCCTTCAGGGTCTGCTTATGCCCTTGTTCAAGAACACCAGTGTGAGCTCT  
CTGTACTCTGGTTGCAGACTGACCTTGCTCAGGCCTGAGAAGGATGGGGCAGCCACCAGAGTGGATGCTG  
TCTGCACCCATCGTCTGACCCCAAAGCCCTGGAAGTGGACAGAGAGCGGCTGTACTGGAAGCTGAGCCA  
GCTGACCCACGGCATCACTGAGCTGGGCCCCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGTTTC  
ACCCATCGGAGCTCTGTACCCACCACCAGCACCGGGTGGTCAGCGAGGAGCCATTCAACCTGCCCGGG  
CGGCCGCTCGA

**29\_16483.edit**

AGCGTGGTCGCGGCCGAGGTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGGG  
TTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTAAGTGTCTGGAATGGGGCCCATGAGA  
TGGTTGTCTGAGAGAGAGCTTCTTGCTCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTG  
GCCGTTGTGGGCGGTGTGGTCCGCCTAAAACCATGTTCCCTCAAAGATCATTTGTTGCCAACACTGGGTTG  
CTGACCAGAAGTGCCAGGAAGCTGAATACCATTTCCAGTGTGATACCCAGGGTGGGTGACGAAAGGGGTC  
TTTTGAACTGTGGAAGGAACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACCAGTTG  
GGGAAGCTCGTCTGTCTTTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATA  
AATTGTATATTCGGTCCCGGTTCCAGGCCAGTAATAGTAGCCTCTGTGACACCAGGGCGGGGCCGAGGGA  
CCCTTCTNTTGAAGAGACCAGCTTCTCATACTTGATGATGAGNCCGGTAATCCTGGCACGTGGNNGGTTGC  
ATGATNCCACCAAGGAAATNGNNGGGGNGGACCTGCCCGGCGGCGTTCNAAAGCCCAATTCCACACA  
CTTGGNNGCGTACTATGATCCCACTCNGTCCAACCTTGGNGGAATATGGCATAACTTTT

**31\_16484.edit**

TCGAGCGGCCGCCCCGGGCAGGTGCTTGACCTTTTCAGCAAGTGGGAAGGTGTAATCCGTCTCCACAGACA  
AGGCCAGGACTCGTTTGTACCCGTTGATGATAGAATGGGGTACTGATGCAACAGTTGGGTAGCCAATCTGC  
AGACAGACACTGGCAACATTGCGGACACCCTCCAGGAAGCGAGAATGCAGAGTTTCTCTGTGATATCAAG  
CACTTCAGGGTTGTAGATGCTGCCATTGTGCAACACCTGCTGGATGACCAGCCCAAAGGAGAAGGGGGAG  
ATGTTGAGCATGTTGAGCAGCGTGGCTTCGCTGGCTCCCACTTTGTCTCCAGTCTTGATCAGACCTCGGCC  
GCGACCACGCT

**37\_16487.edit**

AGCGTGGTCGCGGCCGAGGTCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTG  
CCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGG  
ACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACCTCTG  
GGGGGACCGTCAGTCTTCTCTTCCCCGCATCCCCCTTCAAACCTGCCCGGGCGGCGCTCG

**38\_16487.edit**

CGAGCGGCCGCCCGGGCAGGTTTGAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAGG  
AGTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTTTTGTCACAAGATTTGGGCTCAACTCTCTTGTCCAC  
CTTGGTGTGCTGGGCTTGATCTACGTTGCAGGTGTAGGTCTGGGTGCCGAAGTTGCTGGAGGGCAGC  
GTCACCACGCTGCTGAGGGAGTAGAGTCCTGAGGACTGTAGGACAGACCTCGGCCGCGACCACGCT

**39\_16488.edit**

NGGNNGGTCCGGNCNGNCAGGACCACTCNTCTTCGAAATA

**41\_16489.edit**

AGCGTGGTCGCGGCCGAGGTCCTCACTTGCCTCCTGCAAAGCACCGATAGCTGCGCTCTGGAAGCGCAGA  
TCTGTTTTAAAGTCCTGAGCAATTTCTCGCACCAGACGCTGGAAGGGAAGTTTGCGAATCAGAAGTTCAGT  
GGACTTCTGATAACGTCTAATTTACGGAGCGCCACAGTACCAGGACCTGCCCGGGCGGCCGCTCGA

**42\_16489.edit**

TCGAGCGGCCGCCCGGGCAGGTCCTGGTACTGNGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACT  
GAACTTCTGATTCGCAAACCTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAACAGATCTG  
CGCTTCCAGAGCGCAGCTATCGGTGCTTTGCAGGAGGCAAGTGAGGACCTCGGCCGCGACCACGCT

**45\_16491.edit**

TCGAGCGGCCGCCCGGGCAGGTCCACATCGGCAGGGTTCGGAGCCCTGGCCGCCATACTCGAACTGGAAT  
CCATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCCTTGGGGTTCTTGCTGATGTACCAGTTCTT  
CTGGGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATG  
GCATCCAGGTTGCAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTT  
GAGGTCACGGCAGGTGCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT



46\_16491.edit

GTGGGNTTGAACCCNTTTNANCTCCGCTTGGTACCGAGCTCGGATCCACTAGTAACGGCCGCCAGTGTGC  
TGGAATTCGGCTTAGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATG  
TGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCA  
AAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCCAAGAAGAA  
CTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTC  
CAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGACCTGCCCGGGCGGCCGCTCGA

47\_16492.edit

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAG  
AAACAGGAGGAAATAGCCCTGTCCAGGAGTTCAGTGTGCTGGGAGCAAGTCTACAGCTACCATCAGCGG  
CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCA  
GCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTTCAGG  
ACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCTTACTGGTTACAGAGTAACCACCACTCCCA  
AAAATGGACCAGGACCAACAAAACCTAAACCTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTG  
CAGCCACAGTGGAGTATGTGGTTAAGTGTCTATGCTCAGAATCCAAGCGGAGAGAAGTCAGCCTCTGGTT  
CAGACTGNAAGTAACCAACATTGATCGCCTAAAGGACTGGCATTCACTGATGNGGATGCCGATTCCATCAA  
AATTGNTTGGGAAAACCCACAGGGGCAAGTTTNCANGTCNAGGNGGACCTACTCGAGCCCTGAGGATGGA  
ATCCTTGACTNTTCTTNNCCTGATGGGGAAAAAAACCTTNAAAACCTTGAAGGACCTGCCCGGGCGGCCG  
TNCAAAACCCAATTCCACCCCTTGGGGGCGTTCTATGGGNCCCACTCGGACCAACTTGGGGTAAN

48\_16492.edit

TCGAGCGGCCGCCCCGGGCAGGTCCTTGACAGCTCTGCAGTGTCTTCTTCACCATCAGGTGCAGGGAATAGC  
TCATGGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCCTGTGGGCTTTCCCA  
AGCAATTTTGATGGAATCGGCATCCACATCAGTGAATGCCAGTCCTTTAGGGCGATCAATGTTGGTTACTGC  
AGTCTGAACCAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGG  
GCTGCAAGCCTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTGGTCTGTCCATT  
TTTGGGAGTGGTGGTTACTCTGTAACCAAGTAACAGGGGAACTTGAAGGCAGCCACTTGACACTAATGCTGT  
TGCTCCTGAACATCGGTCACTTGCATCTGGGATGGTTTGTCAATTTCTGTTTCGGTAATTAATGGAAATTGGCT  
TGCTGCTTGCGGGGCTTGTCTCCACGGCCAGTGACAGCATACACAGTGATGGTATAATCAACTCCAGGTTT  
AAGCCGCTGATGGTAGCTGAACTTTGCTCCAGGCACAAGTGAACCTCCTGACAGGGCTATTTCTNCTGTT  
CTCCGTAAGTGATCCTGTAATATCTCACTGGGACAGCAGGANGCATTCCAAAACCTTCGGGCGNGACCCCT  
AAGCCGAATTNTGCAATATNCATCACACTGGCGGGCGCTCGANCATTCAATAAAGGCCCAATCNCCCCTA  
TAGGGAGTNTANTACAATTNG

**49\_16493.edit**

TCGAGCGGCCGCCCCGGGCAGGTCACCTTTGGTTTTGGTCATGTTGGTTGGTCAAAGATAAAAACTAAGT  
TTGAGAGATGAATGCAAAGGAAAAAATATTTCCAAAGTCCATGTGAAATTGTCTCCCATTTTTTTGGCTTT  
TGAGGGGGTTCAGTTTGGGTTGCTTGTCTGTTTCCGGGTTGGGGGGAAGTTGGTTGGGTGGGAGGGAGC  
CAGGTTGGGATGGAGGGAGTTTACAGGAAGCAGACAGGGCCAACGTCG

**55\_16496.edit**

AGCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGACC  
AGCAGAGGCATAAGGTTCTGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCAACC  
TACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCATTATGCCGTTGGAGATGAGTGGGAACGAATGT  
CTGAATCAGGCTTTAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTATCTA  
GATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGACC  
TGCCCCGGGCGGCCGCTCGA

**56\_16496.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAGTTCACAC  
CATTGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACA  
GTTTAAAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA  
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGA  
ACCTTATGCCTCTGCTGGTCTTTCAGTGCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTC  
GGCCGCGACCACGCT

**59\_16498.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCACCATAAGTCCTGATACAACCACGGATGAGCTGTCAGGAGCAAGGT  
TGATTTCTTTCATTGGTCCGGTCTTCTCCTTGGGGGTCACCCGCACTCGATATCCAGTGAGCTGAACATTGG  
GTGGTGTCCACTGGGCGCTCAGGCTTGTGGGTGTGACCTGAGTGAACCTCAGGTCAGTTGGTGCAGGAAT  
AGTGGTTACTGCAGTCTGAACCAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACAT  
ACTCCACTGTGGGCTGCAAGCCTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAGTTTTTGTG  
GTCCTGGTCCATTTTTGGGAGTGGTGGTACTCTGTAACCAGTAACAGGGGAACTTGAAGGCAGCCACTTG  
ACACTAATGCTGTTGTCCTGAACATCGGTCACTTGCATCTGGGATGGTTTGNCAATTTCTGTTCCGTAATTA  
ATGGAAATTGGCTTGCTGCTTGCGGGGCTGTCTCCACGGCCAGTGACAGCATACACAGNGATGGNATNAT  
CAACTCCAAGTTTAAGGCCCTGATGGTAACTTTAACTTGCTCCAGCCAGNGAACTTCCGGACAGGGTAT  
TTCTTCTGGTTTTCCGAAAGNGANCCTGGAATNNTCTCCTTGGANCAGAAGGANCNTCCAAAACCTGGGCC  
GGAACCCCTT

**"REPLACEMENT SHEETS"**

**60\_16473.edit**

AGCGTGGTCGCGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGGG  
TTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGA  
TGGTTGTCTGAGAGAGAGCTTCTTGTCCTACATTCGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGGTG  
GCCGTTGTGGGCGGTGTGGTCCGCCTAAAACCATGTTCTCCTCAAAGATCATTGTTGCCCAACACTGGGTTG  
CTGACCAGAAGTGCCAGGAAGCTGAATACCATTTCCAGTGTACATCCAGGGTGGGTGACGAAAGGGGTC  
TTTTGAACTGTGGAAGGAACATCCAAGATCTCTGGTCCATGAAGATTGGGGTGTGGAAGGGTTACAGTTG  
GGGAAGCTCGTCTGTCTTTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTTCAGGGCAATGACATA  
AATTGTATATTGGTTCCCGGTTCCAGGCCAGTAATAGTAGCCTCTTGTGACACCAGGCGGGGCCANGGA  
CCACTTCTCTGGGANGAGACCCAGCTTCTCATACTTGATGATGTAACCCGGTAATCCTGCACGTGGCGGCT  
GNCATGATACCANCAAGGAATTGGGTGNGGNGGACCTGCCCCGGCGGCCCTCNA

**60\_16498.edit**

AGCGTGGTCGCGGCCGAGGTCCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAG  
AAACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG  
CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCA  
GCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTTACAG  
ACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCA  
AAAATGGACCAGGACCAACAAAACTAAAACTGCAGGTCCAGATCAAACAGAAATGACTATTGAAGGCTTG  
CAGCCCACAGTGGAGTATGTGGTTAGTGTCTATGCTCAGAATCCAAGCGGAGAGAGTCAGCCTCTGGTTCA  
GACTGCAGTAACCACTATTCTGCACCAACTGACCTGAAGTTCACTCAGGTCACACCCACAAGCCTGAGCC  
GCCAGTGGACACCACCAATGTTCACTCACTGGATATCGAGTGCGGGTGACCCCCAAGGAGAAGACCCGG  
ACCCATGAAAGAAATCAACCTTGCTCCTGACAGCTCATCCGNGGGTGTATCAGGACTTATGGGGGACTGCC  
CCGGCNGGCCGNTCGAAANCGAATTNTGAAATTTCTTCNCACTGGGNGGCGNTTCGAGCTTNTNTANA  
NGGCCAATTCNCCTNTAGNGGGTCGTN

**61\_16499.edit**

AGCGTGGTCGCGGCCGAGGTCNAGG

**62\_16483.edit**

TCGAGCGGCCGCGCCGGGCGAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCA  
GGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCGG  
CCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCC  
TGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACC  
CTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTCGTC  
ACCCACCCTGGGTATGACACTGGAAATGGTATTCAGCTTCTGGAAGTCTGTCAGCAACCCAGTGTGG  
GCAACAAATGATCTTTGAGGAACATGGTTTTAGGCGGACCACACCGCCCAACGGGCACCCCAATAAGG  
NATAGGCCAAGACCATACCCCGCCGAATGTAGGACAAGAAGCTCTNTCTCAACAACCATCTCATGGGCCCC  
ATTCCAGGACACTTCTGAGTACATCATTTTATGTCATCCTGGTGGGCACTTGATGAANAACCCCTTACAGTTC  
AGGGTTCCTGGAACCTTCTACCAGNGCCACTTCTGACAGGANCTTGGGCGNGACCACCT

*Fig. 1500*

**63\_16500.edit**

AGCGTGGTCGCGGCCGAGGTCCATTTTCTCCCTGACGGTCCCACTTCTCTCCAATCTTGTAAGTTCACACCA  
TTGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACAGT  
TTAAAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAAACTGTGTAGGGGTCAAAG  
CACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGCCACGGTAACAACCTCTTCCCGAAC  
CTTATGCCTCTGCTGGTCTTTAGTGCCTCCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTGCC  
CGGGCGGCCCGCTCGA

**64\_16493.edit**

AGCGTGGTCGCGGCCGAGGTGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTG  
TAAACTCCCTCCATCCCAACCTGGCTCCCTCCCACCCAACCAACTTTCCCCCAACCCGGAAACAGACAAG  
CAACCCAAACTGAACCCCTCAAAGCCAAAAAATGGGAGACAATTCACATGGACTTTGGAAAATATTTT  
TTTCCTTTGCATTCTCTCAAACCTTAGTTTTTATCTTTGACCAACCGAACATGACCAAAAACCAAAAAGTGA  
CCTGCCCCGGCGGCCGCTCGA

**64\_16500.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCTCACCAGAGGTGCCACCTACAACATCATAGTGGAGGCACTGAAAGA  
CCAGCAGAGGCATAAGGTTGGGAAGAGGTTGTTACCGTGGGCAACTCTGTCAACGAAGGCTTGAACCA  
CCTACGGATGACTCGTGCTTTGACCCCTACACAGTTTCCCATTATGCCGTTGGAGATGAGTGGGAACGAAT  
GTCTGAATCAGGCTTTAAACTGTTGTGCCAGTGCTTAGGCTTTGGAAGTGGTCATTTAGATGTGATTCATC  
TAGATGGTGCCATGACAATGGTGTGAACTACAAGATTGGAGAGAAGTGGGACCGTCAGGGAGAAAATGGA  
CCTCGGCCGCGACACGCT

**16501.edit**

TCGAGCGGCCCGCCGGGCAGGTACCGGGGTGGTCAGCGAGGAGCCATTACACTGAACTTCACCATCAA  
CAACCTGCGGTATGAGGAGAACATGCAGCACCCCTGGCTCCAGGAAGTTCAACACCACGGAGAGGGTCCTT  
CAGGGCCTGCTCAGGTCCCTGTTCAAGAGCACCACTGTTGGCCCTCTGTACTCTGGCTGCAGACTGACTTT  
GCTCAGACCTGAGAAACATGGGGCAGCCACTGGAGTGGACGCCATCTGCACCCTCCGCCTTGATCCCACT  
GGTNCTGGACTGGACANANAGCGGCTATACTTGGGAGCTGANCCNAACCTTTGGCGGNGACNCCNCTT

**16501.2.edit**

GAGGACTGGCTCAGCTCCCAGTATAGCCGCTCTCTGTCCAGTCCAGGACCAGTGGGATCAAGGCGGAGG  
GTGCAGATGGCGTCCACTCCAGTGGCTGCCCATGTTTCTCAAGTCTGAGCAAAGNCAGTCTGCAGCCAG  
AGTACAGAGGGCCAACACTGGTGCTCTTGAACAGGGACCTGAGCAGGCCCTGAAGGACCCTCTCCGTGGT  
GTTGAACTTCCTGGAGCCAGGGTGCTGCATGTTCTCCTCATACCGCAGGTTGTTGATGGTGAAGTTCAGTG  
TGAATGGCTCCTCGCTGACCACCC

**16502.1.edit**

AGCGTGGTCGCGGCCGAGGTCCACCACACCCAATTCCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGG  
ATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCC  
CTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCCTG  
AAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACCCT  
TCCACACCCCAATCTTCATGGACCANANANCTTGGATNGTCCTTTCACNGGTTNAAAAAACCTTTTCGCCC  
CCCCACCTTGGGGATTAACCTTGGGAAANGGGGATTTNACCNTTCC

**16502.2.edit**

TCGAGCGGCCCGCCGGGCAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCAGGAACCCTGAACTGTAAG  
GGTTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGA  
GATGGTTGTCTGAGAGAGAGCTTCTTGTCTACATTGGGCGGGTATGGTCTTGGCCTATGCCTTATGGGGG  
TGGCCGTTGTGGGCGGTGTGGTCCGCCTAAAACCATGTTCTCAAAGATCATTTGTTGCCCAACACTGGGT  
TGCTGACCAGAAGTGCCAGGAAGCTGAATACCATTTCCAGTGTATACCCAGGGNGGGTGACCAAAGGGG  
GTCNTTNGACCTGGNGAAAGGAACCATCCAAAANCTCTGNCCCATG

**"REPLACEMENT SHEETS"**

**16503.1.edit**

AGCGTGGNCGCGGCCGAGGTCTGAGGATGTAACTCTTCCCAGGGGAAGGCTGAAGTGCTGACCATGGT  
GCTACTGGGTCCCTTCTGAGTCAGATATGTGACTGATGNGAACTGAAGTAGGTACTGTAGATGGTGAAGTCT  
GGGTGTCCCTAAATGCTGCATCTCCAGAGCCTTCCATCATTACCGTTTCTTCTTTTCTGCTATGGGATGAGACA  
CTGTTGAGTATTCTCTAAAGTCACTACTGAAATCTTCTCCAAAGGAAAACCTGTGGAAAAGCCCCCTTATTT  
CTGCCCCATAATTTGGTTCTCCTAATCNCCTCTGAAATCACTATTTCCCTGGAANGTTTGGGAAAAANNGGCG  
NACCTGNCANTGGAAANTGGATANAAAGATCCCACCATTTTACCCAACNAGCAGAAAGTGGGAANGGTACC  
GAAAAGCTCCAAGTAANAAAAAGGAGGGAAGTAAAGGTCAAGTGGGCACCAGTTTCAAACAAAACCTTTCCC  
CAAACATANAACCCA

**16503.2.edit**

AAGCGGCCGCCCCGGGCAGGNNCAGNAGTGCCTTCGGGACTGGGNTCACCCCCAGGTCTGCGGCAGTTGT  
CACAGCGCCAGCCCCGCTGGCCTCCAAAGCATGTGCAGGAGCAAATGGCACCGAGATATTCCTTCTGCCA  
CTGTTCTCCTACGTGGTATGTCTTCCCATCATCGTAACACGTTGCCTCATGAGGGTCACACTTGAATTCTCC  
TTTTCCGTTCCCAAGACATGTGCAGCTCATTTGGCTGGCTCTATAGTTTGGGAAAGTTTGTGAAACTGTG  
CCACTGACCTTTACTTCCTCCTTCTCTACTGGAGCTTTCCGTACCTTCCACTTCTGCTGNTGGNAAAAAGGG  
NGGAACNTCTTATCAATTTTATTGGACAGTANCCCNCTTTCTNCCCCAAAACATNCAAGGGAAAAATATTGATT  
NCNAGAGCGGATTAAGGAACAACCCNAATTATGGGGGCCAGAAATAAAGGGGGCTTTTCCACAGGTNTTTT  
CCT

**16504.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTGCAGGCTATTGTAAGTGTTCTGAGCACATATGAGATAACCTGGGCC  
AAGCTATGATGTTTCGATACGTTAGGTGTATTAATGCACTTTTGAAGTCCATCTCAGTGGATGACAGCCTTC  
TCACTGACAGCAGAGATCTTCTCTACTGTGCCAGTGGGCAGGAGAAAGAGCATGCTGCGACTGGACCTCG  
GCCGCGACCACGCT

**16504.2.edit**

AGCGTGGTTCGCGGCCGAGGTCCAGTCGCAGCATGCTCTTTCTCCTGCCCACTGGCACAGTGAGGAAGATC  
TCTGCTGTCAGTGAGAAGGCTGTCATCCACTGAGATGGCAGTCAAAAGTGCATTTAATACACCTAACGTATC  
GAACATCATAGCTTGGCCCAGGTTATCTCATATGTGCTCAGAACACTTACAATAGCCTGCAGACCTGCCCG  
GGCGGCCGCTCGA

**16505.1.edit**

CGAGCGGCCGCCCGGGCAGGTCCAGACTCCAATCCAGAGAACCACCAAGCCAGATGTCAGAAGCTACAC  
CATCACAGGTTTACAACCAGGCACTGACTACAAGATCTACCTGTACACCTTGAATGACAATGCTCGGAGCTC  
CCCTGTGGTCATCGACGCTCCACTGCCATTGATGCACCATCCAACCTGCGTTTCCTGGCCACCACACCCA  
ATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCAGGATTACCGGCTACATCATCAAGTATGAGAAGCCT  
GGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCGCCCTGGTGNCACAGAAGCTACTATTACTGGCCTGG  
AACCGGGAACCGAATATACAATTTATGTCATTGCCCTGAAGAATAATCANAAGAGCGAGCCCCTGATTGGAA  
GG

**16505.2.edit**

AGCGTGGTCGCGGCCGAGGTCCTGTCAGAGTGGCACTGGTAGAAGTTCCAGGAACCCTGAACTGTAAGGG  
TTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGTGTCTGGAATGGGGCCCATGAGA  
TGGTTGTCTGAGAGAGAGCTTCTTGTCCTGTCTTTTCTTCCAATCAGGGGCTCGCTCTTCTGATTATTCTT  
CAGGGCAATGACATAAATTGTATATTCGGTTCCCGGTTCCAGGCCAGTAATAGTAGCCTCTGTGACACCAG  
GGCGGGGCCGAGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGTANCCGGTAAT  
CCTGGCACCGTGGCGGCTGCCATGATACCAGCAAGGAATTGGGTGTGGTGGCCAAGAAACGCAGGTTGG  
ATGGTGCATCAATGGCAGTGGAGGCGTCGATNACCACAGGGGAGCTCCGANCATTGTCATTCAAGGTGGA  
CAGGTAGAATCTTGTAATCAGGTGCCTGGTTTGTAACCTG

**16506.1.edit**

TCGAGCGGCCGCCCGGGCAGGTTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGC  
CAGCAGATCGAGAACATCCGGAGCCCAGAGGGCAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTC  
AAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATG  
CCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCA  
GAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAAGCATGTCTGGTTCCGGCGAAAGCATGACCGAT  
GGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGACCTCGGCCGCGACCACGCT  
AAGCCCGAATTCCAGCACACTGGCGGCCGTTACTAGTGGGATCCGAGCTTCGGTACCAAGCTTGGCGTAA  
TCATGGGNCATAGCTGTTTCCTGNGTGAAAATGGTATTCCGCTTCACAATTTCCCAC

**16506.2.edit**

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCC  
ATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTG  
GGCCAACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCA  
TCCAGGTTGCAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTTGAG  
GTCACGGCAGGTGCGGGCGGGGTTCTTGCGGCTGCCCTCTGGGCTCCGGATGTTCTCGATCTGCTGGCT  
CAAGCTCTTGAAAGGTGGTGTCCACCTCGAGGTCACGGTCACGAAACCTGCCCGGGCGGCCGCTCGA

**"REPLACEMENT SHEETS"**

**16507.1.edit**

AGCGTGGTCGCGGCCGAGGTCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACT  
GGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAAC  
ATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAAGAACTGGTACATCAGCA  
AGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGG  
CGGCCAGGGCTCCGACCCTGCCGATGTGGACCTGCCCGNGCCGNGCCGCTCGAAAAGCCCNAAATTTCCA  
GNCACACTTGGCCGGCCGTTACTACTG

**16507.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCACATCGGCAGGGTCCGAGCCCTGGCCGCCATACTCGAACTGGAAT  
CCATCGGTCTATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTTCTTGCTGATGTACCAGTTCTT  
CTGGGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATG  
GCATCCAGGTTGCAGCCTTGGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTT  
GAGGTCACGGCAGGTGCGGGCGGGGTTCTTGACCTCGGCCGCGACCACGCT

**16508.1.edit**

CGAGCGGCCGCCCCGGGCAGGTCCCCCCCCCTTT  
TTTTTTTTTTTTTTTTTTTT

**16508.2.edit**

AGCGTGGTCGCGGCCGAGGTCTGGCATTCTTCTGACTTCTCTCCAGCCGAGCTTCCCAGAACATCACATAT  
CACTGCAAAAATAGCATTGCATACATGGATCAGGCCAGTGGAATGTAAAGAAGGCCCTGAAGCTGATGGG  
GTCAAATGAAGGTGAATTCAAGGCTGAAGGAAATAGCAAATTCACCTACACAGTTCTGGAGGATGGTTGCA  
CGAAACACACTGGGGAATGGAGCAAAACAGTCTTTGAATATCGAACACGCAAGGCTGTGAGACTACCTATT  
GTAGATATTGCACCCTATGACATTGGTGGTCCTGATCAAGAATTTGGTGTGGACGTTGGCCCTGTTTGCTTT  
TTATAAACCAAACCTCTATCTGAAATCCCAACAAAAAAATTTAACTCCATATGTGNTCCTCTTGTTCTAATCTT  
GGCAACCAGTGCAAGTGACCGACAAAATTCAGTTATTTATTTCCAAAATGTTTGAAACAGTATAATTTGAC  
AAAGAAAAAAGGATACTTCTCTTTTTTTGGCTGGTCCACCAAATACAATTCAAAAGGCTTTTTGGTTTTATTTT  
TTTANCCAATTCCAATTTCAAATGTCTCAATGGNGCTTATAATAAAATAAACTTTCACCCTTNTTTNTGAT



**16509.1.edit**

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAG  
AAACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG  
CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCA  
GCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTTCAGG  
ACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAAGTAACCACCACTCCC  
AAAAATGGACCAGGACCAACAAAACTAAACTGCAGGTCCAGATCAAACAGAAAATGGACTATTGAAGGC  
TTGCAGCCCACAGTGGAAGTATGTGGNTAGGNGTCTATGCTCAGAATCCCAAGCCGGAGAAAGTCAGCCTT  
CTGGTTTAGACTGCAGTAACCAACATTGATCGCCCTAAAGGACTGGNCATTCACTTGGATGGTGGATGTCC  
AATTC

**16509.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTTGCAGCTCTGCAGNGTCTTCTTCACCATCAGGTGCAGGGAATAGC  
TCATGGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCCTGTGGGCTTTCCCA  
AGCAATTTTGATGGAATCGACATCCACATCAGNGAATGCCAGTCCTTTAGGGCGATCAATGTTGGTTACTGC  
AGTCTGAACCAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGG  
GCTGCAAGCCTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGTCTGNCCCA  
TTTTTGGGAAGTGGGGGGTTACTCTGTAACCAAGTAACAGGGGAACTTGAAGGCAGCCACTTGACACTAATG  
CTGTTGCTCTGAACATCGGTCACTTGCATCTGGGGATGGTTTTGACAATTTCTGGTTCCGGCAAATTAATGA  
AATTGGCTTGCTGCTTGCGGGGGCTGNCTCCACGGGCCAGTGACAGCATAC

**16510.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTTGCAGCTCTGCAGTGTCTTCTTCACCATCAGGTGCAGGGAATAGC  
TCATGGATTCCATCCTCAGGGCTCGAGTAGGTCAACCTGTACCTGGAACTTGCCCCTGTGGGCTTTCCCA  
AGCAATTTTGATGGAATCGACATCCACATCAGTGAATGCCAGTCCTTTAGGGCGATCAATGTTGGTTACTGC  
AGTCTGAACCAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGG  
GCTGCAAGCCTTCAATAGTCATTTCTGTTTGATCTGGACCTGCAGTTTTAAGTTTTTGGTGGNCCTGNNCCA  
TTTTTGGGAAGGGGTGGTTACTCTTGTAACCAAGTAACAGGGGAACTTGAAGCAGCCACTTGACACTAATG  
CTGGTGGCCTGAACATCGGTCACTTGCATCTGGGATGGTTTGGTCAATTTCTGTTCCGTAAATTAATGGGAAA  
TTGGCTTACTGGCTTGCGGGGGCTGTCTCCACGGNCAGTGACAAGCATACACAGGNGATGGGTATAATCA  
ACTCCAGGTTTAAGGCCNCTGATGGTA

**16510.2.edit**

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAG  
AAACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG  
CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCA  
GTAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTTCAGG  
ACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGTTCCCCTGTTACTGGTTACAGAGTAACCACCACTCCCA  
AAAATGGGACCAGGACCAACAAAACTAAACTGCANGGTCCAGATCAAACAGAAATGACTATTGAAGGC  
TTGCAGCCCACAGTGGAAGTATGTGGGTTAGTGTCTATGCTCAGAATNCCAAGCGGAGAGAGTCAGCCTCTG  
GTTTCAGACT

**16511.1.edit**

TCGAGCGGCCGCCCGGGCAGGTCAGCGCTCTCAGGACGTCAACCACCATGGCCTGGGCTCTGCTCCTCCT  
CACCTCCTCACTCAGGGCACAGGGTCCTGGGCCAGTCTGCCCTGACTCAGCCTCCCTCCGCGTCCGG  
GTCTCCTGGACAGTCAGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGCTTATGAATTTGTCT  
CCTGGTACCAACAACACCCAGGCAAGGCCCCAACTCATGATTTCTGAGGTCACTAAGCGGCCCTCAGG  
GGTCCCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCANGCT  
GAGGATGANGCTGATTATTACTGGAAGCTCATATGCAGGCAACAACAATTGGGTGTTCCGGCGGAAGGGAC  
CAAGCTGACCGTNCTAAGGTCAAGCCCAAGGCTTGCCCCCTCGGTCACTCTGTTCCACCCCTCCTCTGAA  
GAAGCTTCAAGCCAACAANGNCACACTGGGTGTGTCTCATAAGTGGACTTTCTACCC

**16511.2.edit**

AGCGTGGTCGCGGCCGAGGTCTGTAGCTTCTGTGGGACTTCCACTGCTCAGGCGTCAGGCTCAGGTAGCT  
GCTGGCCGCGTACTTGTTGTTGCTTTGNTTGGAGGGTGTGGTGGTCTCCACTCCCGCCTTGACGGGGGCTG  
CTATCTGCCTTCCAGGCCACTGTCACGGCTCCCGGGTAGAAGTCACTTATGAGACACACCAAGTGTGGCCTT  
GTTGGCTTGAAGCTCCTCAGAGGAGGGTGGGAACAGAGTGACCGAGGGGGCAGCCTTGGGCTGACCTAG  
GACGGTCAGCTTGGTCCCTCCGCCGAACACCCAATTGTTGTTGCCTGCATATGAGCTGCAGTAATAATCAG  
CCTCATCCTCAGCCTGGAGCCCAGAGACNGTCAAGGGAGGCCCGTGTTTGCCAAGACTTGGAAGCCAGAN  
AAGCGATCAGGGACCCCTGAGGGCCGCTTTACNGACCTCAAAAAATCATGAATTTGGGGGGCCTTTGCCT  
GGNGTTGGTTGGTNACCAGNAAAACAAAATTTATAAAGCACCAACGTCACTGCTGGTTTCCAGTGCANG  
AANATGGTGAAGTGAANTGTCC

**16512.1.edit**

AGCGTGGTCGCGGCCGAGGTCCAGCATCAGGAGCCCCGCTTGCCGGCTCTGGTCATCGCCTTTCTTTTT  
GTGGCCTGAAACGATGTCATCAATTGCGAGTAGCAGAACTGCCGTCTCCACTGCTGTCTTATAAGTCTGCA  
GCTTCACAGCCAATGGCTCCCATATGCCAGTTCCTTCATGTCCACCAAAGTACCCGTCTCACCATTACAC  
CCCAGGTCTCACAGTTCTCCTGGGTGTGCTTGCCCGAAGGGAGGTAAGTANACGGATGGTGCTGGTCCC  
ACAGTTCTGGATCAGGGTACGAGGAATGACCTCTAGGGCCTGGGCNACAAGCCCTGTATGGACCTGCCCCG  
GGCGGGCCCGCTCGA

**16512.2.edit**

TCGAGCGGCCGCCCGGGCAGGTCCATACAGGGCTGTTGCCCAGGCCCTAGAGGNCATTCCTTGTACCCT  
GATCCAGAACTGTGGGACCAGCACCATCCGTCTACTTACCTCCCTTCGGGCCAAGCACACCCAGGAGAAC  
TGTGAGACCTGGGGTGTAATGGNGAGACGGGTACTTTGGTGACATGAAGGAACTGGGCATATGGGAGC  
CATTGGCTGNGAAGCTGCANACTTATAAGACAGCAGTGGAGACGGCAGTTCTGCTACTGCGAATTGATGAC  
ATCGTTTCAGGCCACAAAAAGAAAGGCGATGACCANAGCCGGCAAGGCGGGGCTTCCTGATGCTGGACCT  
CGGCCGCCGACCACGCTT

**"REPLACEMENT SHEETS"**

**16514.1.edit**

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCCAGGCAGAGTCTCTGCGTTACAAA  
CTCCTAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCC  
AAAGGCTGCGAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATG  
GCCTGATGATCCACAGCGGAGACCCTGTAACTACTACGTTGACACTGCTGTGCGCCACGTGTTGCTCANA  
CAGGGTGTGCTGGGCATCAAGGTGAAGATCATGCTGCCCTGGGACCCANCTGGCAAAAATGGCCCTTAA  
AACCCCTTGCCNTGACCACGTGAACCATTGTGNGAACCCCAAGATGAANATACTTGCCACCAACCCCA  
TTC

**16514.2.edit**

TCGAGCGGCCGCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGC  
AGGCGGCTCTGGCTTCCCACCCTTCTGTTCTGAGATGGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCA  
CAATGCTCACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCCAGGGCAGCATGAT  
CTTCACCTTGATGCCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAGCAGTGTCAACGTAGTAGTTAA  
CAGGGTCTCCGCTGTGGATCATCAGGCCATCCACAACTTCATGGATTTAGCCCTCTGTCCTCGGAGTTTC  
CCAAAACACCACAACCTCGCCAGCCTTTGGGCCCACTTCTTCATGAATGAAACCGCAGCACACCATTANC  
AAGGCCCTTCCGCACAGGNAAGCCCTTCTAAGGAGTTTGTAAACGCAAAAACTCTTGCTGCGGGCAA  
TGGGCACACAGACCTNTANTNGGACCTTGGNCCGCGAACCACCGCTT

**16515.1.edit**

AGCGTGGTCGCGGCCGAGGTCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCCTGGAAAACCCGG  
ACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAACCTCTGGACTTCCT  
GGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGGACAGCCCGGTGCTCCTGGTGTGA  
AGGGTGAACCTGGNGCCCCTGGTGAAAATGGAACCTCAGGTCAAACAGGAGCCCGNGGGCTTCTGGNG  
AGAGAGGACGTGTTGGTGCCCTGGCCANACCTGCCCGGGCGGCGCTCNAAAAGCCGAAATCCAGNA  
CACTGGCGGCCGNTACTANTGGAATCCGAACCTCGGTACCAAAGCTTGGCCGTAATCATGGCCATAGCTTG  
TTCCCTGGGGNGGAAATTGGTATTCCGCTNCCAATTCCACACAACATACCGAACCCGAAAGCATTAAAGT  
GTAAAAGCCCTGGGGGGCCCTAAATGANGTGAGCNTAACTCNCATTTAATTGGCGTTGCGCTTCACTGCC  
CGCTTTTCCAGTCCGGGNA

**16515.2.edit**

TCGAGCGGCCGCCCGGGCAGGTCTGGGCCAGGGGCACCAACACGTCCTCTCTCACCAGGAAGCCACGG  
GCTCCTGTTTGACCTGGAGTTCCATTTTACCAGGGGCACCAGTTTACCCTTACACCAGGAGCACCGG  
GCTGTCCCTTCAATCCATCCAGACCATTGTGNCCCCTAATGCCTTTGAAGCCAGGAAGTCCAGGAGTTCCA  
GGGAAACCACGAGCACCTGTGGTCCAACAACCTCTCTCACCAGGTCGTCCGGGTTTTCCAGGGTGAC  
CATCTTACCAGCCTTGCCAGGAGGGCCAGACCTCGGCCGCGACACGCT

**"REPLACEMENT SHEETS"**

**16516.1.edit**

ANCGTGGTCGCGGCCGAGGTCCTCACCAGAGGTGNCACCTACAACATCATAGTGGAGGCACTGAAAGACC  
ANCAGAGGCATAAGGTTCGGGAAGAGG

**16516.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCATTTCTCCCTGACGGTCCCCTTCTCTCCAATCTTGTAGTTCACAC  
CATTGTCATGGCACCATCTAGATGAATCACATCTGAAATGACCACTTCCAAAGCCTAAGCACTGGCACAACA  
GTTTAAAGCCTGATTGAGACATTCGTTCCCACTCATCTCCAACGGCATAATGGGAACTGTGTAGGGGTCAA  
AGCACGAGTCATCCGTAGGTTGGTTCAAGCCTTCGTTGACAGAGTTGTCCACGGTAACAACCTCTTCCCGA  
ACCTTATGCCTCTGCTGGTCTTTCAGTGCCCTCACTATGATGTTGTAGGTGGCACCTCTGGTGAGGACCTC  
NGNCCNGAACAACGCTTAAGCCCGNATTCTGCAGAATAATCCCATCACACTTGGCGGCCGCTTCGANCATG  
CATCNTAAAAGGGGGCCCCAATTTCCCCCTTATAAGNGAANCCGTATTTNCCAATTTCACTGGNCCCGCCGN  
TTTTACAAACGNCGGTGAAGTGGGGAAAAACCCTGGCGGTTACCCAACCTTTAATCGCCNTTGGCAGCACAA  
TCCCCCTTTTCGNCCANCNTGGGCGTAAATAACCGAAAA

**16517.1.edit**

ANCGNGGTGCGCGCCGANGTNTTTTTCTTNTTTTTT

**16518.1.edit**

AGCGTGGTCGCGGCCGAGGTCTGAGGTTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT  
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC  
AACAGCACGTACCGGGNGGTCAGCGTCCTACCGTCCTGCACCAGAATTGGTTGAATGGCAAGGAGTACA  
AGNGCAAGGTTTCCAACAAAGCCNTCCAGCCCCCNTCGAAAAAACCATTTCCAAAGCCAAAGGGCAGCC  
CCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAAAAGANCAANAACCNGGTTCAGCCTTAA  
CTTGCTTGGTCNAANGCTTTTTATCCCAACGNACTTCCCCCNTGGAANTGGGAAAAACCAATGGGCCAANC  
CGAAAAACAATTACAANAACCCC

**16518.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCT  
GCCCATTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCAGGCAGGTGAGGCTGAC  
CTGGTTCTTGGTCATCTCCTCCCGGGATGGGGGCAGGGTGAACACCTGGGGTTCTCGGGGCTTGCCCTTT  
GGTTTTGAANATGGTTTTCTCGATGGGGCTGGAAGGGCTTTGTTGNAAACCTTGCACTTGACTCCTTGCC  
ATTCACCCAGNCCTGGNGCAGGACGGNGAGGACNCTNACCACACGAACCGGGCTGGTGGACTGCTCC

**16519.1.edit**

AGCGTGGTCGCGGACGANGTCCTGTCAGAGTGGNACTGGTAGAAGTTCCANGAACCTGAACTGTAAGGG  
TTCTTCATCAGTGCCAACAGGATGACATGAAATGATGTACTCAGAAGNGNCCTGGAATGGGGCCCATGANA  
TGGTTGCC

**16519.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCA  
GGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCG  
CCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCC  
TGAAGAATAATCAGAAGAGCGAGCCCCTGATTGGAAGGAAAAAGACAGACGAGCTTCCCCAACTGGTAACC  
CTTCCACACCCCAATCTTCATGGACCAGAGATCTTGGATGTTCTTCCACAGTTCAAAGACCCCTTTCGGC  
ACCCCCCTGGGTATGAACCTGGGAAAANGGNANTTAANCTTTCCTGGCA

**16520.1.edit**

AGCGTGGTCGCGGCCGAGGTCTGGGATGCTCCTGCTGTACAGTGAGATATTACAGGATCACTTACGGAG  
AAACAGGAGGAAATAGCCCTGTCCAGGAGTTCACTGTGCCTGGGAGCAAGTCTACAGCTACCATCAGCGG  
CCTTAAACCTGGAGTTGATTATACCATCACTGTGTATGCTGTCACTGGCCGTGGAGACAGCCCCGCAAGCA  
GCAAGCCAATTTCCATTAATTACCGAACAGAAATTGACAAACCATCCCAGATGCAAGTGACCGATGTTTCAAG  
ACAACAGCATTAGTGTCAAGTGGCTGCCTTCAAGGTNCCCTGGTACTGGGTACAGANTAACCACCACTCC  
CAAAAATGGACCAGGAACCACAAAACCTTAACTGCAGGGTCCAGATCAAAACAGAAATGACTATTGAANG  
CTTGACGCCACAGTGGGAGTATGNGGGTAGTGNCTATGCTTCAGAAATCCAAGCGGAAAAANGTCAAGCC  
TTNTGGGTTCAA

**16520.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTTGACAGCTCTGCAGTGTCTTCTTACCATCAGGTGCAGGGAATAGC  
TCATGGATTCCATCCTCAGGGCTCGAGTAGGTACCCCTGTACCTGGAACTTGCCCCTGTGGGCTTTCCCA  
AGCAATTTTGATGGAATCGACATCCACATCAGTGAATGCCAGTCCTTTAGGGCGATCAATGTTGGTTACTGC  
AGNCTGAACCAGAGGCTGACTCTCTCCGCTTGGATTCTGAGCATAGACACTAACCACATACTCCACTGTGG  
GCTGCAANCCTTCAATAANNCATTTCTGTTTGATCTGGACC

**16521.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTGGTGGGGTCTGGCACACGCACATGGGGGNGTTGNTCTNATCCAG  
CTGCCAGCCCCCATTTGGCGAGTTTGAGAAGGTGTGCAGCAATGACAACAANACCTTCGACTCTTCTCTGCC  
ACTTCTTTGCCACAAAGTGCAACCTGGAGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACTACATCGG  
GCCTTGCAAATACATCCCCCCTTGCCTGGACTCTGAGCTGACCGAATCCCCCTTGCGCATGCGGGACTG  
GCTCAAGAACCGTCCTGGCACCCCTTGTATGANAGGGATGAAGACACNACCC

**16522.1.edit**

AGCGTGGTCGCGGCCGAGGTCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTG  
CCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGG  
ACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG  
GGGGGACCGTCAGTCTTCCTCTTCCCCCGCATCCCCCTTCCAAACCTGCCCCGGGCGGCCGCTCGAAAGCC  
GAATTCCAGCACACTGGCGGCCGGTACTAGTGGANCCNAACCTTGGNANCCAACCTGGNGGAANTAATGGG  
CATAANCTGTTTCTGGGGGGAAATTGGTATCCNGTTTACAATTCCCNCAACAACATACGAGCCGGAAGCATA  
AAAGNGTAAAAGCCTGGGGGNGGCCTANTGAAGTGAAGCTAACTCACATTAATTNGCGTTGCCGCTCACT  
GGCCCGCTTTTCCAGC

**16522.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTTTGGAAGGGGGATGCGGGGGAAGAGGAAGACTGACGGTCCCCCAG  
GAGTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTTTTGTCAAGATTTGGGCTCAACTCTCTTGTCCA  
CCTTGGTGTGCTGGGCTTGTGATCTACGTTGCAGGTGTAGGTCTGGGNGCCGAAGTTGCTGGAGGGCAC  
GGTCACCACGCTGCTGAGGGAGTAGAGTCCTGAGGACTGTANGACAGACCTCGGCCGNGACCACGCTAA  
GCCGAATTCTGCAGATATCCATCACACTGGCGGCCGCTCCGAGCATGCATTTTAGAGG

**16523.1.edit**

AGCGTGGNCGCGGACGANGACAACAACCCC

**16523.2.edit**

TCGAGCGGCCGCCCCGGGCAGGNCCACATCGGCAGGGTCCGAGCCCTGGCCGCCATACTCGAACTGGAAT  
CCATCGGTCATGCTCTTGCCGAACCAGACATGCCTCTTGTCTTGGGGTTCTTGCTGATGNACCAGTTCTT  
CTGGGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATG  
GCATCCAGGTTGCAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAGTGGCACATCTT  
GAGGTCACGGCAGGTGCGGGCGGGGTTCTTGACCT

**16524.1.edit**

AGCGTGGTCGCGGCCGAGGTCCAGCCTGGAGATAANGGTGAAGGTGGTGCCCCCGGACTTCCAGGTATA  
GCTGGACCTCGTGGTAGCCCTGGTGAGAGAGGTGAACTGGCCCTCCAGGACCTGCTGGTTTCCCTGGTG  
CTCCTGGACAGAATGGTGAACCTGGNGGTAAAGGAGAAAGAGGGGCTCCGGNTGANAAAGGTGAAGGAG  
GCCCTCCTGNATTGGCAGGGGGCCCCANGACTTAGAGGTGGAGCTGGCCCCCTGGCCCCGAAGGAGGAA  
AGGGTGCTGCTGGTCCTCCTGGGCCACCTGG

**16524.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTGGGCCAGGAGGACCAATAGGACCAGTAGGACCCCTTGGGCCATCT  
TTCCCTGGGACACCATCAGCACCTGGACCGCCTGGTTCACCCCTTGTCACCCCTTTGGACCAGGACTTCCAAG  
ACCTCCTCTTTCTCCAGGCATTCTTGCAGACCAGGAGTACCANCAGCACCCAGGTGGCCCAGGAGGACCA  
GCAGCACCCCTTTCTCCTTCGGGACCAGGGGGACCAGCTCCACCTCTAAGTCCTGGGGCCCCCTGCCAATC  
CAGGAGGGCCTCCTTCACCTTTCTCACCCGGAGCCCTCTTTCT

**16526.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCACCGGGATATTCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAAC  
GAGAAGGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTTTACCTGGACAGAGTGAGGAGCCTGGAGA  
CCGACAACCGGAGGCTGGAGAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCAGGTCAGAGACT  
GGAGCCATTACTTCAAGATCATCGAGGACCTGAGGGCTCANATCTTCGAAATACTGCNGACAATGCCCG

**16526.2.edit**

ATGCGNGGTGCGGGCCGANGACCANCTCTGGCTCATACTTGACTCTAAAGNCNTCACCAGNANTTACGGN  
CATTGCCAATCTGCAGAACGATGCGGGCATTGTCCGCANTATTTGCGAAGATCTGAGCCCTCAGGNCCTCG  
ATGATCTTGAAGTAANGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTGCTC  
TCCAGCCTCCGGTTCTCGGTCTCCAAGNCTTCTCACTCTGTCCAGGAAAAGAGGCCAGGCGGNCGATCAG  
GGCTTTTGCATGGACT

**16527.1.edit**

AGCGTGGTCGCGGCCGAGGTTGTACAAGCTTT  
TT

**16527.2.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTGCCAACACCAAGATTGGCCCCCGCCGCATCCACACAGTTNGTGTG  
CGGGGAGGTAACAAGAAATACCGTGCCCTGAGGNTGGACGNNGGGAATTTCTCCTGGGGCTCAGAGTGTT  
GTA CTGTA AAAACAAGGATCATCGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCC  
TGGTGAAGAATTGCATCGTGCTCATNGACAGCACACCGTACCGACAGTGGGTACCGAAGTCCCACTATGCN  
CCT

**16528.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTCCACCACACCCAATTCTTGCTGGTATCATGGCAGCCGCCACGTGCCA  
GGATTACCGGCTACATCATCAAGTATGAGAAGCCTGGGTCTCCTCCCAGAGAAGTGGTCCCTCGGCCCCG  
CCCTGGTGTACAGAGGCTACTATTACTGGCCTGGAACCGGGAACCGAATATACAATTTATGTCATTGCCC  
TGAAG

**16528.2.edit**

AGCGTGNTCNCGGCCGAGGATGGGGAAGCTCGNCTGTCTTTTTCTTCCAATCAGGGGCTNNNTCTTCTG  
ATTATTCTTCAGGGCAANGACATAAATTGTATATTCGNTCCCGGTTCCAGNCCAGTAATAGTAGCCTCTGT  
GACACCAGGGCGGGGCCGAGGGACCACTTCTCTGGGAGGAGACCCAGGCTTCTCATACTTGATGATGAAG  
CCGGAATCCTGGCACGTGGGCGGCTGCCATGATACCACCAANGAATTGGGTGTGGTGGACCTGCCCGG  
GCGGGCCGCTCGAAAANCCGAATTCNTGCAAGAATATCCATCACACTTGGGCGGGCCGNTCGAACCATGC  
ATCNTAAAAGGGCCCCAATTTCCCCCTATTAGNGAAGCCNCATTTAACAATTCCAATTGG

**16529.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTCTCGCGGTGCACTGGTGATGCTGGTCCTGTTGGTCCCCCGGCCCT  
CCTGGACCTCCTGGTCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTC  
AAGAGAAGGCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTTCGTGACCGTGACCT  
CGAGGTGGACACCACCTCAAGAGCCTTGAGCCAGCAGAATCGAAAACATTCGGAACCCAAGAAGGGCAA  
GCCCGCAAAGAAACCCCGCCGACCTGGCCGNGAACCTCCAAGAANGTGCCACANTCTTGACTGGGAAA  
AAAAGGGAAAANTACTTGGAATTGGAC

**16529.2.edit**

AGCGTGGTCGCGGCCGAGGTCCACATCGGCAGGGTCGGAGCCCTGGCCGCCATACTCGAACTGGAATCC  
ATCGGTCATGCTCTCGCCGAACCAGACATGCCTCTTGCTCTTGGGGTTCTTGCTGATGTACCAGTTCTTCTG  
GGCCACACTGGGCTGAGTGGGGTACACGCAGGTCTCACCAGTCTCCATGTTGCAGAAGACTTTGATGGCA  
TCCAGGTTGCAGCCTTGTTGGGGTCAATCCAGTACTCTCCACTCTTCCAGTCAGAAGTGGCACATCTTGA  
GGTCACGGCAGGGTGCGGGCGGGGTTCTTGCGGGCTGCCCTTCTGGGCTCCCGGAATGTTCTNNGAACT  
TGCTGG



**16530.1.edit**

AGCGTGGTCGCGGCCGAGGTCCACTAGAGGTCTGTGTGCCATTGCCAGGCAGAGTCTCTGCGTTACAAA  
CTCCTAGGAGGGCTTGCTGTGCGGAGGGCCTGCTATGGTGTGCTGCGGTTTCATCATGGAGAGTGGGGCC  
AAAGGCTGCGAGGTTGTGGTGTCTGGGAACTCCGAGGACAGAGGGCTAAATCCATGAAGTTTGTGGATG  
GCCTGATGATCCACAGCGGAGACCCTGTAACTACTACGTTGACACTTGCTTGTGCGCCACGTGTTGCTCA  
NACANGGGTGGGCTGGGCATCAAGNG

**16530.2.edit**

TCGAGCGGCCGCCCGGGCAGGTCTGCCAAGGAGACCCTGTTATGCTGTGGGGACTGGCTGGGGCATGGC  
AGGCGGCTCTGGCTTCCACCCCTTCTGTTCTGAGATGGGGGTGGTGGGCAGTATCTCATCTTTGGGTTCCA  
CAATGCTCACGTGGTCAGGCAGGGGCTTCTTAGGGCCAATCTTACCAGTTGGGTCCCAGGGCAGCATGAT  
CTTCACCTTGATGCCCAGCACACCCTGTCTGAGCAACACGTGGCGCACAGCAAGTGTCAACGTAAGTAAGT  
TAACAGGGTCTCCGCTGTGGATCATCAGGCCATCCACAACTTCATGGATTAAACCCTCTGTCTCGGAG

**16531.1.edit**

TCGAGCGGCCGCCCGGGCAGGTGTTTCAGAGGTTCCAAGGTCCACTGTGGAGGTCCCAGGAGTGCTGGT  
GGTGGGCACAGAGGTCCGATGGGTGAAACCATTGACATAGAGACTGTTCTGTCCAGGGTGTAGGGGCC  
AGCTCTTTGATGCCATTGGCCAGTTGGCTCAGCTCCCAGTACAGCCGCTCTCTGTTGAGTCCAGGGCTTTT  
GGGGTCAAGATGATGGATGCAGATGGCATCCACTCCAGTGGCTGCTCCATCCTTCTCGGACCTGAGAGAG  
GTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTCTTTGAATA

**16531.2.edit**

AGCGTGGTCGCGGCCGAGGTCTGTACTGGGAGCTAAGCAAACCTGACCAATGACATTGAAGAGCTGGGCCC  
CTACACCCTGGACAGGAACAGTCTCTATGTCAATGGTTTACCCATCAGAGCTCTGTGNCCACCACCAGCA  
CTCCTGGGACCTCCACAGTGGATTTCAGAACCTCAGGGACTCCATCCTCCCTCTCCAGCCCCACAATTATG  
GCTGCTGGCCCTCTCCTGGTACCATTACCCTCAACTTCACCATCACCAACCTGCAGTATGGGGAGGACAT  
GGGTACCCTGNCTCCAGGAAGTTCAACACCACA

**16532.1.edit**

TCGAGCGGCCGCCCGGACAGGTCTGGGCGGATAGCACCGGGCATATTTTGAATGGATGAGGTCTGGCA  
CCCTGAGCAGTCCAGCGAGGACTTGGTCTTAGTTGAGCAATTTGGCTAGGAGGATAGTATGCAGCACGGN  
TCTGAGNCTGTGGGATAGCTGCCATGAAGTAACCTGAAGGAGGTGCTGGCTGGTANGGGTTGATTACAGG  
GTTGGGAACAGCTCGTACACTTGCCATTCTCTGCATATACTGGTTAGTGAGGTGAGCCTGGCCCTCTTCTTT  
TG

**"REPLACEMENT SHEETS"**

**01\_16558.3.edit**

AGCGTGGTCGCGGCCGAGGTGAGCCACAGGTGACCGGGGCTGAAGCTGGGGCTGCTGGNCCTGCTGGT  
CCTG

**02\_16558.4.edit**

CAGCNGCTCCNACGGGGCCTGNNGGACCAACAACACCGTTTTTACCCTTAGGCCCTTTGGCTCCTCTTTCT  
CCTTTAGCACCAGGTTGACCAGCAGCNCCANCAGGACCAGCAAATCCATTGGGGCCAGCAGGACCGACCT  
CACCACGTTACCCAGGGCTTCCCCGAGGACCAGCAGGACCAGCAGGACCAGCAGCCCCAGCTTCGCCCC  
GGTCACCTGTGGCTCACCTCGGCCGCGACCACGCT

**03\_16535.1.edit**

TCGAGCGGTCGCCCCGGGCAGGTCCACCGGGATAGCCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAA  
CGAGAAGGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGAGGAGCCTGGA  
GACCGANAACCGGAGGCTGGANAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCCAGGTCAAGAG  
ACTGGAGCCATTACTTCAAGATCATCGAGGGACCTGGAGG

**04\_16535.2.edit**

AGCGNNGGTCGCGGCCGAGGTCCAGCTCTGTCTCATACTTGACTCTAAAGTCATCAGCAGCAAGACGGGCA  
TTGTCAATCTGCAGAACGATGCGGGCATTGTCCGCAGTATTTGCGAAGATCTGAGCCCTCAGGTCCTCGAT  
GATCTTGAAGTAATGGCTCCAGTCTCTGACCTGGGGTCCCTTCTTCTCCAAGTGCTCCCGGATTTTGCTCTC  
CAGCCTCCGGTTCTCGGTCTCCAGGCTCCTCACTCTGTCCAGGTAAGAAGGCCAGGCGGTGTTTCAGGC  
TTTGCATGGTCTCCTTCTCGTTCTGGATGCCTCCCATTCTGCCAGACCC

**05\_16536.1.edit**

TCGAGCGGCCGCCCCGGGCAGGTGAGGAAGCACATTGGTCTTAGAGCCACTGCCTCCTGGATTCCACCTGT  
GCTGCGGACATCTCCAGGGAGTGAGGAAGGGAAGCAGGTCAAAGTCTGCTCAGATCAGTCAGACTGGCTGTT  
CTCAGTTCTCACCTGAGCAAGGTCAGTCTGCAGCCAGAGTACAGAGGGCCAACACTGGTGTTCTTGAACAA  
GGGCTTGAGCAGACCCTGCAGAACCTCTTCCGTGGTGTGAACTTCCTGGAAACCAGGGTGTTGCATGTT  
TTTCCTCATAATGCAAGGTTGGTGATGG

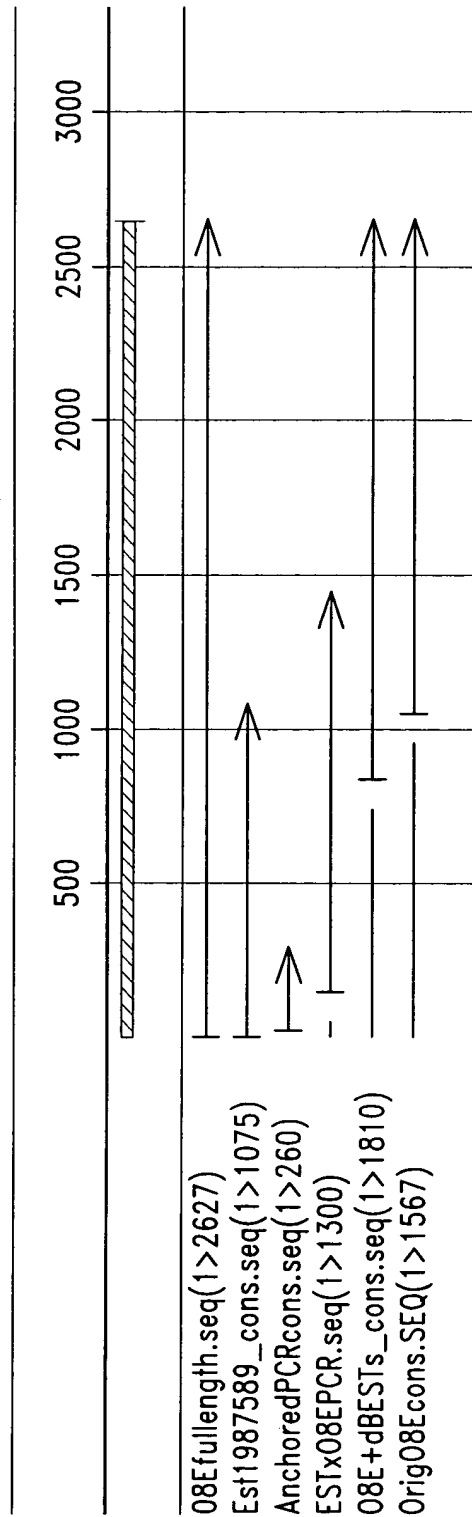
*Fig. 15DDD*

**07\_16537.1.edit**

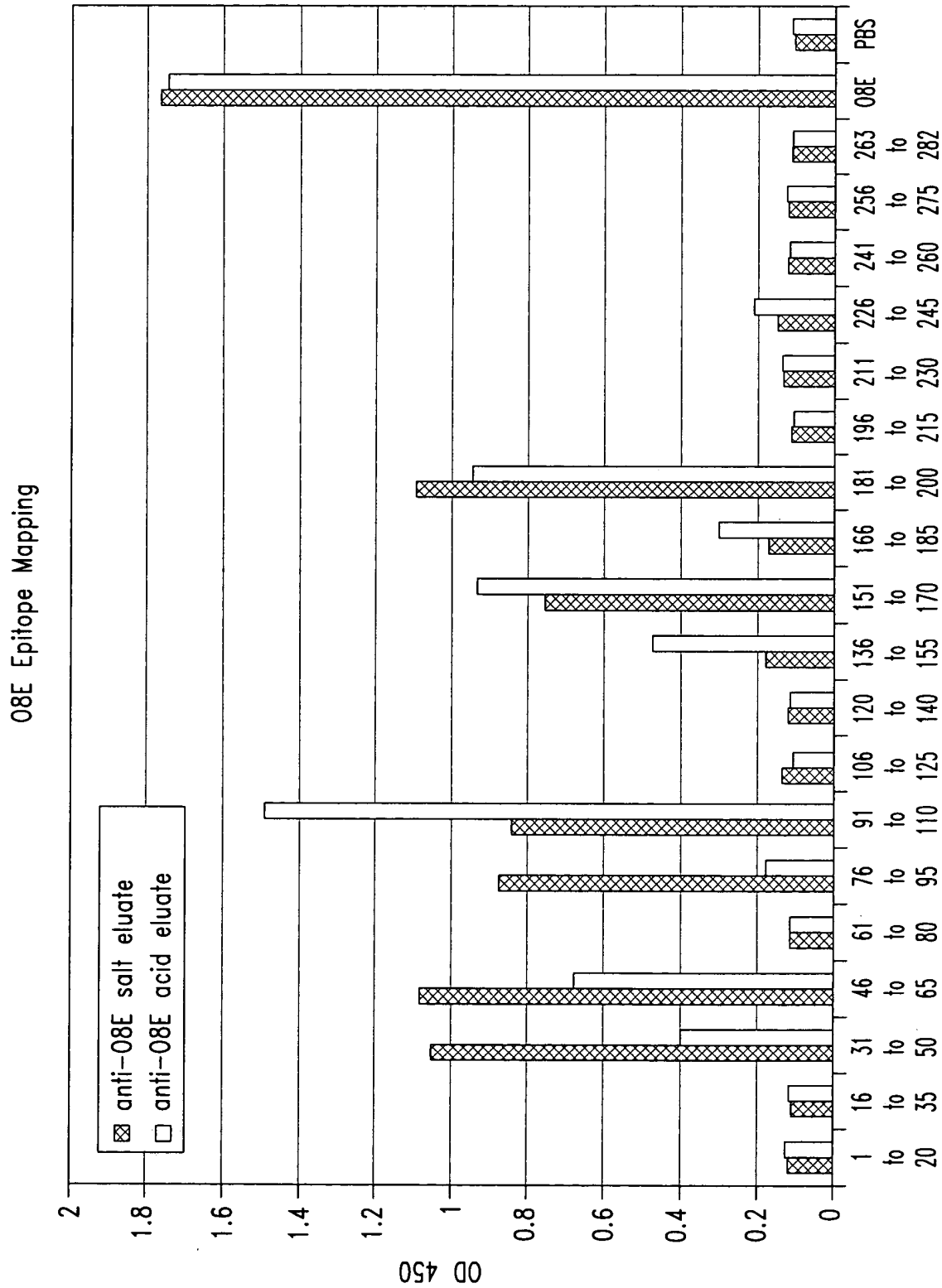
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CCCGCTCGA

**08\_16537.2.edit**

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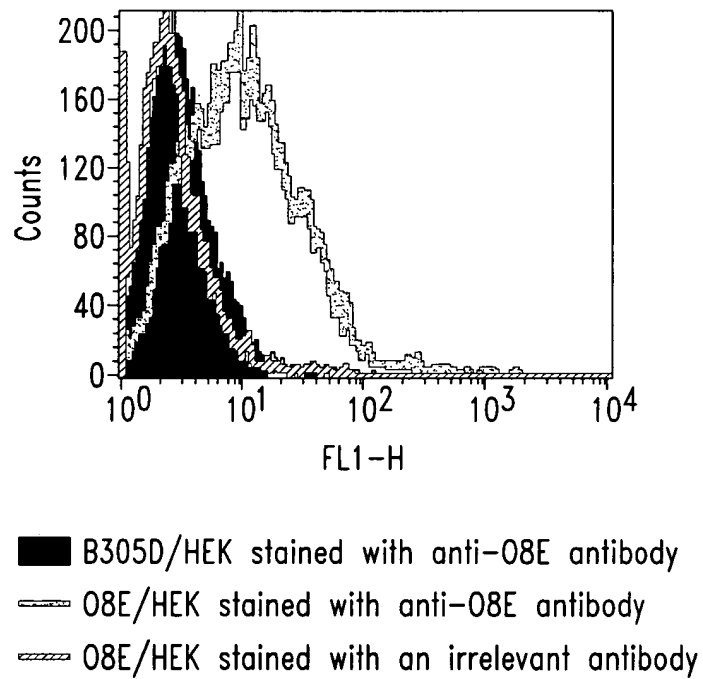


*Fig. 16*

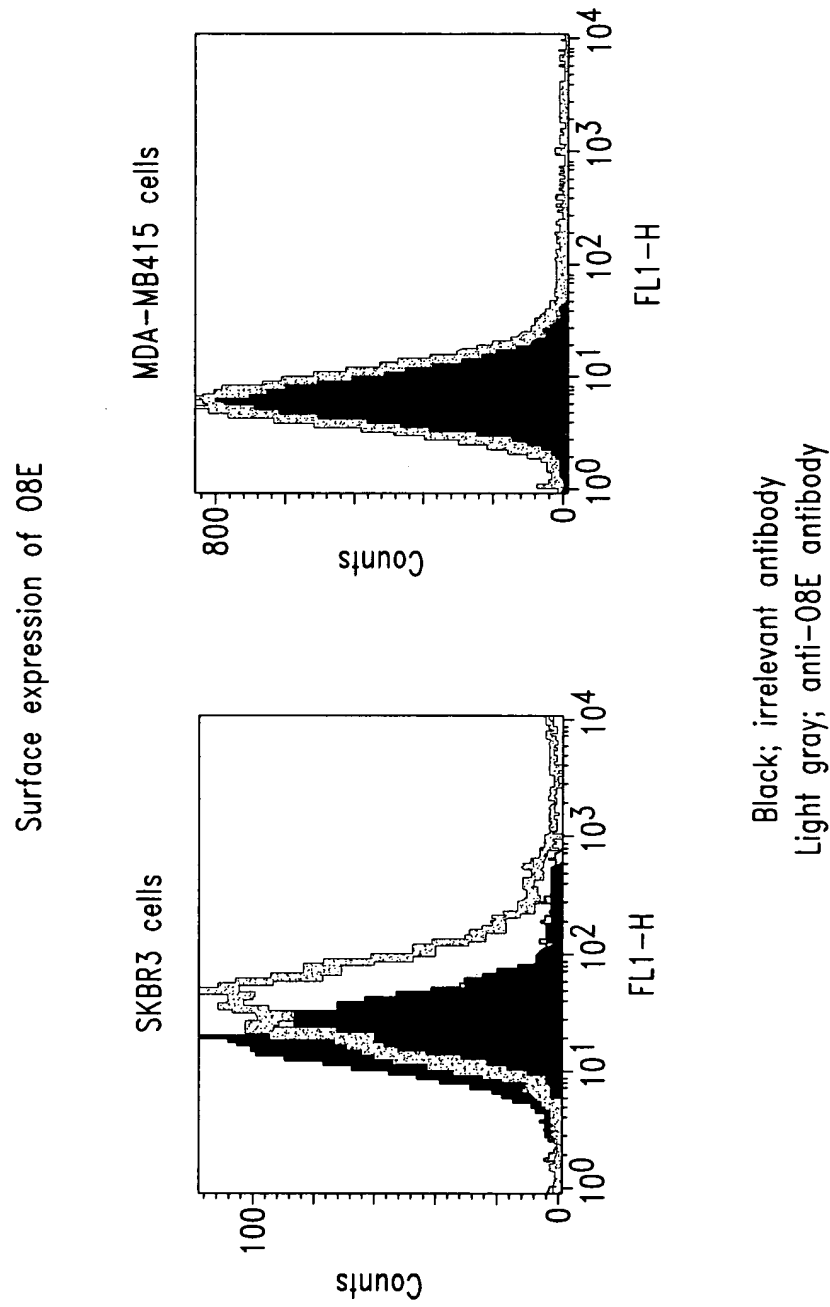


*Fig. 17*

O8E Surface Expression

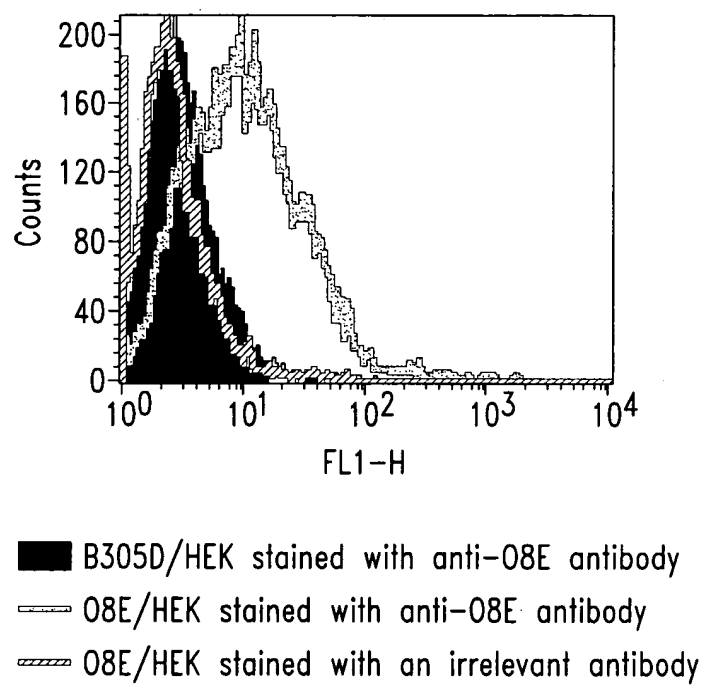


*Fig. 18*



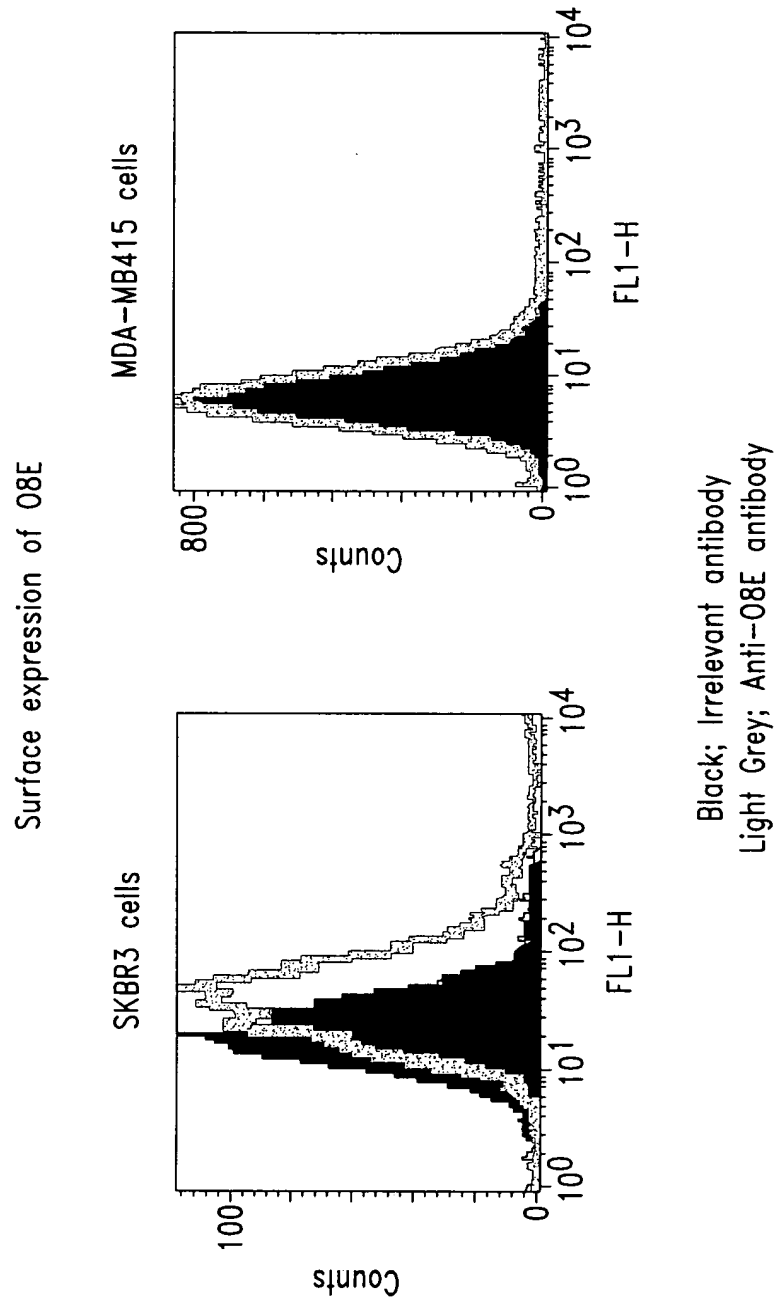
*Fig. 19*

O8E Surface Expression



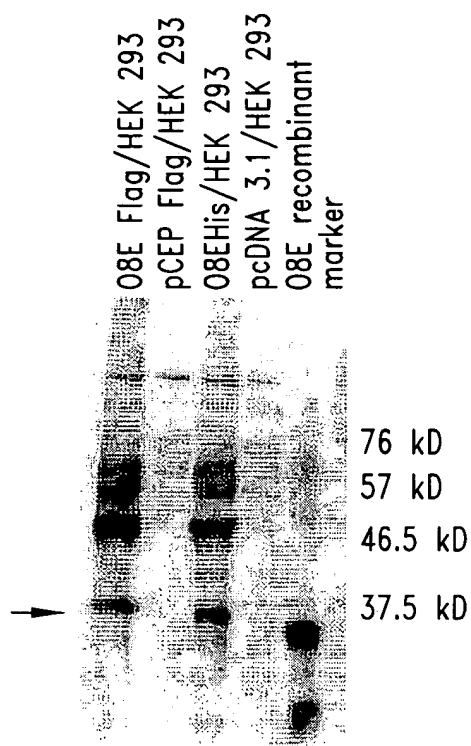
*Fig. 20*





*Fig. 21*

O8E expression in HEK293 Cells  
(probed with anti-O8E rabbit polyclonal sera #2333L)



*Fig. 22*

08E Rabbits 01212000

Date: 1/21/99

Antigen on Plate	Sera Sample	Antibody Dilutions													
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000	1:4096000	1:8192000
08E (#632-24)	Preimmune sera (#2576L):11/10/99	0.13	0.09	0.08	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.07	0.07	0.07	0.07
	Average	0.10	0.08	0.07	0.07	0.07	0.07	0.07	0.06	0.06	0.07	0.06	0.06	0.07	0.07
	$\alpha$ -08E (#2576K):1/11/2000	2.92	2.81	2.74	2.70	2.58	2.08	1.61	1.01	0.68	0.40	0.24	0.15	0.15	0.15
	Average	2.93	2.77	2.74	2.69	2.48	2.08	1.57	1.00	0.66	0.40	0.23	0.16	0.16	0.16
	Preimmune sera (#2333L):11/10/99	0.09	0.07	0.06	0.06	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	Average	0.08	0.07	0.06	0.07	0.10	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	$\alpha$ -08E (#2333L):1/11/2000	2.73	2.75	2.64	2.48	2.30	1.78	1.41	0.92	0.58	0.32	0.20	0.14	0.14	0.14
	Average	2.73	2.76	2.51	2.60	2.37	1.93	1.44	0.88	0.58	0.35	0.20	0.14	0.14	0.14
	Average	2.73	2.76	2.57	2.54	2.33	1.85	1.43	0.90	0.58	0.33	0.20	0.14	0.14	0.14

Fig. 23

affi-pure O8E #2576L 739.87A&B

Antibody Name		Date: 5/2/2000	
Rabbit #, Bleed Date	O8E polyclonal 2576L, 1/11/2000		
Purification Method	affinity		
Buffer	PBS		
Notebook	#705, p150		
lot #	739.87A	739.87B	
Antibody Concentration	1.4mg/ml	1.7mg/ml	
Initial Amount	18mg	3mg	

Antigen on Plate	Sera Sample	Antibody Dilutions											
		1:1000	1:2000	1:4000	1:8000	1:16000	1:32000	1:64000	1:128000	1:256000	1:512000	1:1024000	1:2048000
O8E #632-24	preimmune sera (2576L)	0.15	0.11	0.09	0.08	0.08	0.07	0.07	0.07	0.07	0.08	0.07	0.08
	Average	0.14	0.10	0.09	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07
	$\alpha$ -O8E (2576K):2/8/2000	2.74	2.71	2.63	2.49	2.29	1.87	1.39	0.92	0.57	0.33	0.20	0.14
	Average	2.72	2.68	2.64	2.47	2.26	1.93	1.42	0.94	0.57	0.34	0.21	0.14
	affinity pure $\alpha$ -O8E poly	2.73	2.70	2.63	2.48	2.27	1.90	1.41	0.93	0.57	0.34	0.21	0.14
	salt peak 739-87A	2.69	2.60	2.50	2.21	1.83	1.34	0.99	0.64	0.38	0.22	0.15	0.11
Average	Average	2.59	2.48	2.38	2.21	1.82	1.33	1.00	0.62	0.37	0.22	0.14	0.11
	affinity pure $\alpha$ -O8E poly	2.64	2.54	2.44	2.21	1.83	1.34	1.00	0.63	0.37	0.22	0.15	0.11
	acid peak 739-67B	2.46	2.39	2.40	2.34	2.08	1.73	1.29	0.81	0.49	0.29	0.19	0.13
	Average	2.65	2.66	2.61	2.45	2.14	1.76	1.30	0.82	0.48	0.29	0.19	0.13
Average		2.56	2.53	2.51	2.39	2.11	1.74	1.30	0.81	0.49	0.29	0.19	0.13

Fig. 24

Anti-O8E mAb Binding to O8E Amino Acids  
61-80 Induces Ligand Internalization

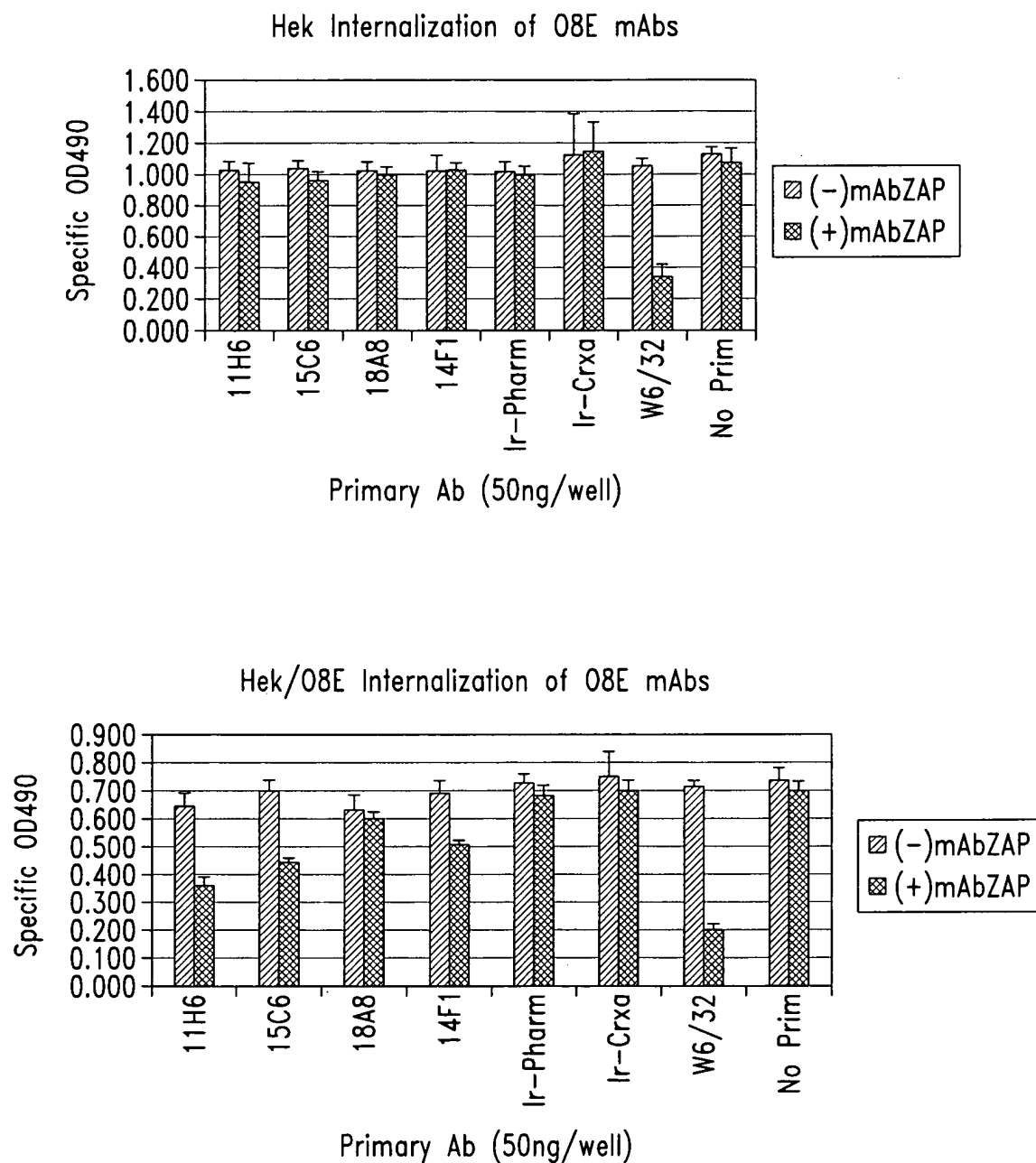


Fig. 25